

GenCore version 5.1.7									
OM protein - protein search, using sw model									
Run on: April 3, 2006, 08:02:30 ; Search time 81 Seconds (without alignments) 86.791 Million cell updates/sec									
Title:	US-09-647-457P-3	Score:	90	Sequence:	1 LWNGLCTCQIKKGpac	Scoring table:	BLOSUM62	Database:	Gapop 10.0 , Gapext 0.5
Searched:	2443163 seqs, 439378781 residues	Total number of hits satisfying chosen parameters:	2443163	Minimum DB seq length:	0	Maximum DB seq length:	200000000	Post-processing:	Minimum Match 0%
Maximum Match 100% Listing first 100 summaries									
Database :	A_Geneseq_21:*	*							
1:	geneseqp1980s:*								
2:	geneseqp1906s:*								
3:	geneseqp2000s:*								
4:	geneseqp2018s:*								
5:	geneseqp2002s:*								
6:	geneseqp2003s:*								
7:	geneseqp2003bs:*								
8:	geneseqp2004s:*								
9:	geneseqp2005s:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description	Match	Length	DB ID	Score	Detail
1	90	100.0	16	2 AAY43191	Aay3191 Schizoph	74	65	65	ADZ170522
2	78	86.7	16	2 AAY43204	Aay3204 Schizoph	75	65	72.2	434 9 AEB116803
3	78	86.7	17	2 AAY43198	Aay3198 Schizoph	76	61	67.8	438 2 AAY43200
4	78	86.7	17	2 AAY43197	Aay3197 Schizoph	77	59	65.6	432 7 ADD263377
5	74	82.2	458	6 AAGT9784	Aagt9784 Carbohydr	78	59	65.6	434 9 AEB119158
6	74	82.2	458	8 ADQ30526	Adq0526 Pancreas	79	59	65.6	434 9 AEB116885
7	74	82.2	458	9 ADW08691	Adw08691 Human pro	80	58	64.4	15 2 AAY43203
8	65	72.2	16	2 AAY43202	Aay3202 Schizoph	81	56	62.2	395 9 AEB116875
9	65	72.2	17	2 AAY43196	Aay3196 Schizoph	82	56	62.2	434 8 ADN254563
10	65	72.2	18	2 AAY43195	Aay3195 Schizoph	83	56	62.2	437 9 ADY174633
11	65	72.2	19	2 AAY43194	Aay3194 Schizoph	84	55	61.1	433 4 ABB107632
12	65	72.2	20	2 AAY43193	Aay3193 Schizoph	85	51	56.7	66 5 ABB107632
13	65	72.2	28	2 AAY43192	Aay3192 Schizoph	86	51	56.7	68 3 AAG201665
14	65	72.2	50	2 ADU78952	Adu78952 Human pro	87	51	55.7	77 3 AAG201655
15	65	72.2	156	8 ADT31055	Adt31055 Cancer re	88	51	56.7	78 3 AAG201644
16	65	72.2	269	6 ABU04377	Abu04377 Human exp	89	51	56.7	2 11 8 ADX95179
17	65	72.2	269	9 ADZ03357	Adz03357 Human pro	90	51	56.7	45 8 ADX95179
18	65	72.2	272	6 ABU04378	Abu04378 Human exp	91	51	56.7	313 7 ABB109093
19	65	72.2	272	6 ABU04375	Abu04375 Human exp	92	51	56.7	340 7 ADM67652
20	65	72.2	336	6 ABU04376	Abu04376 Human exp	93	51	56.7	342 7 AAG201655
21	65	72.2	420	6 AAE39225	Aae39225 Human enz	94	51	56.7	443 7 ABB173339
22	65	72.2	429	3 AAB402064	Aab402064 Human ORP	95	51	56.7	444 3 AAG335522
23	65	72.2	429	6 ABU03938	Abu03938 Human exp	96	51	56.7	449 3 AEA10001
24	65	72.2	433	2 AAW14001	AAW14001 Endolase p	97	51	56.7	449 3 AAG335511

Raw53357	Alpha	Endo	Abu03944	Human	exp
			Abu03942	Human	exp
			Adq30574	Pancreas	
			Abb57379	Rat	mucoc
			Abp5147	Hypoxia- <i>r</i>	
			Abp6155	Hypoxia- <i>r</i>	
Abr6211	Angiogene				
Abr4746	Breast	ca			
Abr57704	Human	eno			
Abu03943	Human	exp			
Abu03934	Human	exp			
Abu03936	Human	exp			
Abu03935	Human	exp			
Abu03932	Human	exp			
Abu03930	Human	exp			
Abu03931	Human	exp			
Abu03937	Human	exp			
Abu03933	Human	exp			
Abm04797	Human	alp			
Adb81166	Rat	enolase			
Adc27709	Human	alp			
Adp8355	Human	pro			
Adf76365	Novel	hum			
Adn95644	Human	BEC			
Adp51133	Human	eno			
Adp51165	Antipori				
Adp2542	Protein	e			
Ado19151	Human	PRO			
Adq18898	Human	sof			
Adq19129	Human	sof			
Adg76748	Human	eno			
Adg76750	Human	eno			
Adq6746	Human	eno			
Abm0012	Tumour- <i>as</i>				
Abm1339	Tumour- <i>as</i>				
Adp54197	Human	PRO			
Adp23174	PRO	polyp			
Adw23363	Human	hep			
Ady9632	PRO	polyp			
Ady70135	Brain	tum			
Adz70552	Human	PRO			
Abel6877	Rat	neuro			
Abel6883	Human	neu			
Abel6875	Rat	neuro			
Abel6884	Rat	neuro			
Abel6885	Human	neu			
Abay34523	Enolase	1			
Abay3200	Schizophr				
Add6937	Human	adi			
Abi51198	Chicken	9			
Abi6886	Chicken	n			
Aav43203	Schizophr				
Adt17141	Trichinel				
Adn2854	Bacterial				
Ady71463	Trichinel				
Abc95179	Drosophil				
Abp54165	Human	hyd			
Aag20166	Arribidops				
Aag20155	Arribidops				
Ag01614	Arribidops				
Adx97369	Plant	ful			
Abm09093	Rice	abio			
Adm7652	D.	salina			
Ag37553	Arribidops				
Abm3839	DNA	clone			
Aab37552	Arribidops				
Aae60820	Arribidops				
Ag37551	Arribidops				



XX  
PS Claim 3; Page 21; 37pp; English.  
XX  
CC This sequence is a peptide of the invention, which binds antibodies found  
CC in elevated levels in body fluids of schizophrenic patients. The peptide  
CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
CC peptide to a platelet-containing fraction of blood, or a fraction  
CC containing platelet-associated antibodies (PAA) shed from the platelets,  
CC or preferably whole blood. The new peptides are able to differentiate  
CC between plasma samples from schizophrenic and non-schizophrenic patients,  
CC and can do so without having to first isolate the platelet-associated  
CC antibodies (PAA) fraction.  
XX  
SQ Sequence 17 AA:  
XX  
Query Match 86.7%; Score 78; DB 2; Length 17;  
Best Local Similarity 93.8%; Pred. No. 0.00094; 0; Mismatches 1; Indels 0; Gaps 0;  
Matches 15; Conservative  
OY 1 LWVGLCTQKIKTGAC 16  
ID AAG79784 standard; protein; 458 AA.  
Db 1 LWVGLCTQKIKTGAC 16  
AC AAG79784;  
XX DT 16-APR-2003 (first entry)  
XX DE Carbohydrate-associated protein (CHOP)-6.  
XX KW Human; carbohydrate associated polypeptides; CHOP; cancer;  
KW carbohydrate metabolism; diabetes; anaemia; hypoglycaemia; obesity;  
KW glycogen storage disease; neurological dysfunction; gene therapy;  
KW cell proliferation; actinic keratosis; arteriosclerosis; inflammation;  
KW atherosclerosis; cirrhosis; hepatitis; psoriasis; autoimmune disorder;  
KW Addison's disease; allergy; asthma; contact dermatitis; bronchitis; gout;  
KW Hashimoto's thyroiditis; infection; reproduction; endometriosis;  
KW poly cystic ovary syndrome; ovarian hyperstimulation syndrome;  
KW Down syndrome; cystic fibrosis; sickle cell anaemia; thalasssemia;  
KW myocarditis; cardiomopathy; Alzheimer's disease; Parkinson's disease;  
KW dementia; depression; epilepsy; Tourette's disorder; schizophrenia;  
KW central nervous system; cerebral palsy; mood; anxiety; knockin;  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
DE Peptide 1. .455  
XX FT /label= "Enolase  
KW Peptide /note= "Identified by BLAST\_DOMO"  
OS WO951725-A2. 1. .293  
XX FT /label= Enolase lyse  
FT /note= "Identified by BLAST\_DOMO"  
FT Peptide 2. .456  
FT /label= Enolase  
FT /note= "Identified by HMMER\_PFAM"  
FT Peptide 2. .456  
FT /label= Enolase  
FT /note= "Identified by BLAST\_DOMO"  
FT Peptide 7. .456  
FT /label= Enolase  
FT /note= "Identified by BLAST\_DOMO"  
FT Protein 35. .57  
FT /label= Enolase  
FT /note= "Identified by BLAST\_DOMO"  
FT Peptide 38. .52  
FT /label= Enolase signature  
FT /note= "Identified by BLIMPS\_PRINTS"  
FT Peptide 113. .129  
FT /label= Enolase signature  
FT /note= "Identified by BLIMPS\_PRINTS"  
FT Protein 153. .202  
FT /label= Enolase protein  
FT /note= "Identified by BLIMPS\_BLOCKS"  
FT Peptide 173. .185  
FT /label= Enolase signature  
FT /note= "Identified by BLIMPS\_PRINTS"  
FT Protein 229. .271  
FT /label= Enolase protein  
FT /note= "Identified by BLIMPS\_BLOCKS"  
FT Peptide 275. .440  
FT /label= Lyase magnesium enolase  
FT /note= "Identified by BLAST\_DOMO"  
FT Protein 302. .315  
FT /label= Enolase protein  
FT /note= "Identified by BLIMPS\_BLOCKS"  
FT Peptide 314. .362  
FT /label= Enolase signature  
XX Sequence 17 AA;  
XX  
Query Match 86.7%; Score 78; DB 2; Length 17;  
Best Local Similarity 93.8%; Pred. No. 0.00094; 0; Mismatches 1; Indels 0; Gaps 0;  
Matches 15; Conservative

CC naturally occurring genomic sequences  
 XX SQ Sequence 458 AA:  
 Query Match Best Local Similarity 82.2%; Score 74; DB 6; Length 458;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 L V W G I C T C O K I G P A C 16  
 Db 407 I V W E I C T G O I K I G P T C 422

FT /note= "Identified by PROFILESCAN"  
 FT 331..366  
 FT /label= Enolase protein  
 FT /note= "Identified by BLIMPS\_BLOCKS"  
 FT 335..346  
 FT /label= Enolase signature  
 FT /note= "Identified by BLIMPS\_PRINTS"  
 FT 361..375  
 FT /label= Enolase signature  
 FT /note= "Identified by BLIMPS\_BLOCKS"  
 FT 392..409  
 FT /label= Enolase signature  
 FT /note= "Identified by BLIMPS\_PRINTS"  
 FT 403..441  
 FT /label= Enolase protein  
 FT /note= "Identified by BLIMPS\_BLOCKS"  
 FT 408..456  
 FT /label= Enolase lyase glycolysis  
 FT /note= "Identified by BLAST\_PRODOM"  
 XX WO200297060-A2.  
 PN XX PD 05-DEC-2002.  
 XX PP 22-MAY-2002; 2002WO-US018354.  
 PR 25-MAY-2001; 2001US-0293768P.  
 PR 01-AUG-2001; 2001US-0309548P.  
 PR 23-AUG-2001; 2001US-0314400P.  
 PR 19-OCT-2001; 2001US-0343706P.  
 PR 07-DEC-2001; 2001US-0337999P.  
 PR XX PD 01-JUL-2004.  
 PR XX PR 11-DEC-2003; 2003WO-BP014057.  
 PR XX PR 17-DEC-2002; 2002EP-00028058.  
 PR 05-NOV-2003; 2003EP-00025237.  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (SINO-) SINOCOMMAX CO LTD CHINESE NAT HUMAN GEN.  
 XX PI Chen J, Hu L, Liu TH, Liu ZH, Sheen Y;  
 XX DR WPI; 2004-488121/46.  
 XX PT New specific markers comprises at least one polypeptide up-regulated in  
 PT pancreatic cancer, useful for diagnosing pancreatic cancer.  
 XX PS Claim 1; SEQ ID NO 13; 381PP; English.  
 CC The sequences given in AAC77779..98 represent human carbohydrate  
 CC associated polypeptides (CHOP). The CHOP polypeptides and the nucleotide  
 CC sequences encoding them are useful for diagnosing, treating and  
 preventing cancer, carbohydrate metabolic disorders (e.g. diabetes,  
 CC anaemia, hypoglycemia, obesity, glycogen storage disease, neurological  
 CC dysfunction), cell/proliferative disorders (e.g. actinic keratosis,  
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis),  
 CC autoimmune/inflammatory disorders (such as acquired immunodeficiency  
 CC syndrome (AIDS), Addison's disease, allergies, asthma, contact  
 CC dermatitis, bronchitis, gout, Hashimoto's thyroiditis), viral, bacterial,  
 CC fungal, parasitic, protozoal and helminthic infections, reproductive  
 CC disorders (e.g. endometriosis, polycystic ovary syndrome, ovarian  
 CC hyperstimulation syndrome), genetic disorders (e.g. Down syndrome, cystic  
 CC fibrosis, sickle cell anaemia, thalassemia), cardiac disorders (e.g.  
 CC myocarditis, cardiomyopathy), neurological disorders (e.g. Alzheimer's  
 CC disease, Parkinson's disease), dementia, depression, epilepsy, Tourette's  
 CC disorder, schizophrenia), and developmental disorders of central nervous  
 CC system (e.g. cerebral palsy), mental disorders (e.g. mood, anxiety). CHOP  
 CC proteins are useful in a number of drug screening techniques, and to  
 analyse the proteome of a tissue or cell type. CHOP cDNA is useful for  
 creating "knockin" humanized animals or transgenic animals to model human  
 CC diseases, in somatic or germline gene therapy, to generate a transcript  
 CC image of a tissue or cell type, for detecting differences in the  
 CC chromosomal location due to translocation, inversion, etc., among normal,  
 CC carrier or affected individuals, and as hybridization probes for mapping  
 CC Sequence 458 AA;

CC Query Match Best Local Similarity 82.2%; Score 74; DB 8; Length 458;  
 CC Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVNGLCTCQIKTGpac 16  
 ||||| |||||  
 XX ADW08691 standard; peptide; 422

RESULT 7  
 ID ADW08691; standard; protein; 458 AA.  
 XX  
 AC ADW08691;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 28.  
 XX KW gene targeting; hepatitis C virus infection; protein deactivation;  
 KW protein activation.  
 XX OS Homo sapiens.  
 XX PN EP1493750-A2.  
 XX PD 05-JAN-2005.  
 XX PP 28-JUN-2004; 2004BP-00015098.  
 XX PR 30-JUN-2003; 2003GB-00015248.  
 XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX PT Berndt P, Kilby PM, Rugman P;  
 XX DR WPI; 2005-050476/06.  
 XX PT New targets for an antiviral compound having at least one down- and up-  
 regulated hepatitis C virus (HCV) polypeptide, useful in predicting  
 PT outcomes, treating or preventing HCV infections.  
 XX PS Claim 1; SEQ ID NO 28; 34pp; English.  
 XX CC The invention comprises the amino acid sequences of protein targets for  
 CC anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the  
 invention are either up-regulated or down-regulated in HCV-infected  
 CC tissue. The proteins of the invention are useful in the preparation of a  
 medicament for the treatment or prevention of HCV infection. The present  
 CC amino acid sequence represents a human protein of the invention which is  
 CC down-regulated in HCV-infected tissue.  
 XX SQ Sequence 458 AA;

Query Match 82.2%; Score 74; DB 9; Length 458;  
 Best Local Similarity 87.5%; Pred. No. 0.056; Mismatches 14; Conservative 0;  
 Matches 1; Indels 0; Gaps 0;

QY 1 LVNGLCTCQIKTGpac 16  
 ||||| |||||  
 DB 407 LVNGLCTCQIKTGpac 422

RESULT 8  
 ID AAY43202  
 XX AAY43202 standard; peptide; 16 AA.  
 AC AAY43202;  
 XX DT 11-JAN-2000 (first entry)  
 XX DE Schizophrenic derived antibody binding epitope #6.  
 XX KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KW platelet-associated antibody; diagnosis.  
 OS Synthetic.  
 XX PN W09951725-A2.  
 XX PD 14-OCT-1999.  
 XX PP 30-MAR-1999; 99WO-IL000190.  
 XX PR 02-APR-1998; 98IL-00123925.  
 XX PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX PI Shinitzky M, Deckmann M;  
 DR WPI; 1999-611037/52.

PT New Peptides useful for diagnosis of schizophrenia.  
 XX PS Claim 3; Page 21; 37pp; English.

XX  
 CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction  
 SQ Sequence 17 AA;

Query Match

Score 65;

DB 2;

Length 17;

Best Local Similarity 81.2%; Pred. No. 0.056; Mismatches 0; Indels 3; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16  
 Db 1 LVVGLCTCQIKTGAPC 16

RESULT 10

AY43195 ID AYY43195 standard; peptide; 18 AA.

AC XX AYY43195;

DT 11-JAN-2000 (first entry)

XX DE Schizophrenic derived antibody binding epitope #5.

XX KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 XX platelet-associated antibody; diagnosis.

XX OS Synthetic.

XX PN WO951725-A2.

XX PD 14-OCT-1999.

XX PR 30-MAR-1999; 99WO-IL000190.

XX PA (YEDA ) YEDA RES &amp; DEV CO LTD.

XX PI Shinitzky M, Deckmann M;

XX DR WPI; 1999-611037/52.

XX PT New peptides useful for diagnosis of schizophrenia.

XX RS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide  
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction

SQ Sequence 19 AA;

Query Match 72.2%; Score 65; DB 2; Length 19;  
 Best Local Similarity 81.2%; Pred. No. 0.062; Mismatches 0; Indels 3; Gaps 0;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16  
 Db 3 LVVGLCTCQIKTGAPC 16

RESULT 12

AY43193 ID AYY43193 standard; peptide; 20 AA.

AC XX AYY43193;

DT 11-JAN-2000 (first entry)

XX DE Schizophrenic derived antibody binding epitope #3.

XX KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 XX platelet-associated antibody; diagnosis.

XX OS Synthetic.

XX PN WO951725-A2.

Query Match 72.2%; Score 65; DB 2; Length 18;  
 Best Local Similarity 81.2%; Pred. No. 0.059; Mismatches 0; Indels 3; Gaps 0;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16  
 Db 1 LVVGLCTCQIKTGAPC 16

XX  
PD 14-OCT-1999.  
XX  
PF 30-MAR-1999; 99WO-IL000190.  
PR 02-APR-1998; 98IL-00123925.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Shinitzky M, Deckmann M;  
DR WPI; 1999-611037/52.  
XX  
PT New peptides useful for diagnosis of schizophrenia.  
PS Claim 3; Page 21; 37pp; English.  
XX  
CC This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction  
CC Sequence 28 AA;  
SQ

Query Match	72.2%	Score	65;	DB	2;	Length	28;
Best Local Similarity	81.2%	Pred. No.	0.086;	Mismatches	0;	Indels	0;
Matches	13;	Conservative				Gaps	0;

Qy 1 LVVGLCIGQIKGAPC 16  
Db 4 LVVGLCIGQIKGAPC 19

RESULT 13

ID AAY43192 standard; peptide; 28 AA.  
XX  
AC AAY43192;  
DT 11-JAN-2000 (first entry)  
XX  
DE Schizophrenic derived antibody binding epitope #2.  
XX  
KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
KW platelet-associated antibody; diagnosis.  
XX  
OS Synthetic.  
XX  
PN WO991725-A2.  
XX  
PD 14-OCT-1999.  
XX  
PP 30-MAR-1999; 99WO-IL000190.  
PR 02-APR-1998; 98IL-00123925.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PI Shinitzky M, Deckmann M;  
DR WPI; 1999-611037/52.  
XX  
PT New peptides useful for diagnosis of schizophrenia.  
PS Claim 3; Page 21; 37pp; English.  
XX  
CC This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction  
CC Sequence 28 AA;  
SQ

Query Match	72.2%	Score	65;	DB	2;	Length	28;
Best Local Similarity	81.2%	Pred. No.	0.086;	Mismatches	0;	Indels	0;
Matches	13;	Conservative				Gaps	0;

Qy 1 LVVGLCIGQIKGAPC 16  
Db 12 LVVGLCIGQIKGAPC 27

RESULT 14

ID ADU78952 standard; protein; 50 AA.  
XX  
AC ADU78952;  
DT 27-JAN-2005 (first entry)  
XX  
DB Human protein fragment, SEQ ID 325.  
XX  
KW Neuroprotective; Anti-depressant; Neuroleptic; Tranquilizer;  
KW Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;  
KW Cardiovascular Gen.; Antiarteriosclerotic; Antilithemic;  
KW Alzheimer's disease; neurological disorder; phosphatase; enzyme.  
XX  
OS Homo sapiens.  
PN US2004226056-A1.  
XX  
PD 11-NOV-2004.  
XX  
PP 09-FEB-2004; 2004US-00776013.  
XX  
PR 22-DEC-1998; 98US-0113534P.  
PR 12-MAR-1999; 99US-0124120P.  
PR 30-JUN-1999; 99US-0141243P.  
PR 21-DEC-1999; 99US-0046139.  
PR 17-OCT-2000; 2000US-0240790P.  
PR 13-JUN-2001; 2001US-0304775P.  
PR 10-SEP-2001; 2001US-0094904.  
PR 12-OCT-2001; 2001US-0097072.  
PR 15-JUL-2002; 2002US-00194967.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
PT Roch J, Bartel P, Heichman K;  
XX  
DR WPI; 2004-794772/78.

PT Selecting agents useful for treating Alzheimer's disease comprises contacting focal adhesion kinase 2 with a test agent and measuring a biological activity related to focal adhesion kinase 2 function with or without the test agent.  
XX  
PS Disclosure; SEQ ID NO 325; 247pp; English.  
XX  
CC The present invention relates to a method for selecting agents that are potentially useful for the treatment of Alzheimer's disease. The method comprises contacting Focal Adhesion Kinase 2 (FAK2) with a test agent and measuring a biological activity related to FAK2 function in the presence and absence of the test agent. The method is useful for screening compounds or agents that can be used to treat neurological disorders, ailments and diseases including mild cognitive impairment, depression, schizophrenia, obsessive-compulsive disorder, bipolar disorder, and

CC neurodegenerative diseases and disorders and motor neuron diseases and  
 CC disorders such as Alzheimer's disease, Parkinson's disease, dementia with  
 CC Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease,  
 CC Alpers' disease, Leigh's disease, Pelizaeus-Merzbacher disease,  
 CC Olivopontocerebellar atrophy, Friedreich's ataxia, leukodystrophies, Rett  
 CC syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as  
 CC for treating or preventing other diseases such as dyslipidemia, diabetes,  
 CC obesity, cardiovascular diseases such as atherosclerosis and coronary  
 CC heart disease. Also disclosed is the coding sequence for a novel human  
 CC phosphatase called PN7740 (ADUR8628 and ADUR8629). PN7740 contains a  
 CC protein phosphatase 2C domain, which likely acts to dephosphorylate  
 CC specific phospho-serine or phospho-threonine residues on particular  
 CC protein substrates. Although the precise role played by protein  
 CC phosphatase 2Cs in Alzheimer's disease pathogenesis has yet to be  
 CC defined, the inventors have discovered that fragment of PN7740 interact  
 CC with the first phosphotyrosin binding domain (PTB) domain of Fe65 (also  
 CC known as ABB1(10) or amyloid beta (A<sub>4</sub>) precursor protein-binding  
 CC family B, member 1, isoform E9 (710)), suggesting that PN7740 may well be  
 CC involved somehow. Fe65 is known to interact with the cytosolic C-terminal  
 CC region of Amyloid beta (A<sub>4</sub>) precursor protein (APP) and APP metabolism is  
 CC critical to the pathogenesis of Alzheimer's disease, because it leads to  
 CC the release of either toxic Abeta or trophic secreted APP (sAPP)  
 CC metabolites. The present sequence is a potentially useful agent for  
 XX Alzheimer's disease.

SQ Sequence 50 AA;

Query	Match	Score	DB	Length
Best Local Similarity	72.2%	65	8	50
Matches	13; Conservative	0;	Mismatches	3;
			Indels	0;
			Gaps	0;
QY	1 LVNGLCTCQIKKGpac	16		
Db	24 LVNGLCTGQIKKGAPC	39		

RESULT 15

ADTS1055 standard; protein; 156 AA.

AC ADTS1055;

DT 13-JAN-2005 (first entry)

DE Cancer related protein sequence #218.

KW cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung; ovarian; prostate; cancer.

OS Homo sapiens.

XX WO2004092338-A2.

XX PD 28-OCT-2004.

XX PF 12-APR-2004; 2004WO-US111104.

XX PR 11-APR-2003; 2003US-0462399P.

XX PR 01-JUL-2003; 2003US-0484333P.

PA (DIAD-) DIADEXUS INC.

XX Macina RA, Turner LR, Sun Y, Tam A;

XX WPI; 2004-766851/75.

PT New cancer specific nucleic acid (CASNA) molecules, useful for  
 PT diagnosing, monitoring the presence of, or treating a patient with  
 PT breast, colon, lung, ovarian, or prostate cancer.

XX PS Claim 12; SEQ ID NO 359; 891pp; English.

CC The invention relates to an isolated nucleic acid molecule (I)

CC selectively hybridizing to, or comprising at least 95% sequence identity  
 CC to, any of the 362 nucleotide sequences fully defined in the  
 CC specification. The nucleic acid molecules and polypeptides are useful for  
 CC diagnosing, monitoring the presence of, or treating a patient with  
 CC breast, colon, lung, ovarian, or prostate cancer. This sequence  
 CC corresponds to a protein of the invention.

SQ Sequence 156 AA;

Query	Match	Score	DB	Length
Best Local Similarity	81.2%	65	8	156
Matches	13; Conservative	0;	Mismatches	3;
			Indels	0;
			Gaps	0;
QY	1 LVNGLCTCQIKKGpac	16		
Db	106 LVNGLCTGQIKKGAPC	121		

RESULT 16

ID ABU04377 standard; protein; 269 AA.

AC ABU04377;

XX DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #11043.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

PP 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0293544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0359985P.

XX PA (ZYCO-) ZYCOS INC.

XX PT Chicz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX PS Example 2; SEQ ID NO 1043; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

XX Sequence 269 AA;

Query Match 72.2%; Score 65; DB 6; Length 269;  
 Best Local Similarity 81.2%; Pred. No. 0; 6; Mismatches 0;保守性  
 Matches 13; Indels 3; Gaps 0;  
 QY 1 LVVGLCITCQIKTGAPC 16  
 Db 219 LVVGLCITCQIKTGAPC 234

RESULT 17

AD270357  
 ID AD270357 standard; protein; 269 AA.  
 XX  
 AC AD270357;  
 XX  
 DT 30-JUN-2005 (first entry)

DE Human protein from lung cancer marker gene ENO1, SEQ ID 42.  
 DE KW Tumor marker; lung tumor; cytostatic; neoplasm; expression;  
 DE DNA microarray.  
 DE OS Homo sapiens.  
 DE XX WO2005032495-A2.

PD 14-APR-2005.  
 XX  
 PP 01-OCT-2004; 2004WO-US034163.

PR 03-OCT-2003; 2003US-0508335P.  
 PA (FARB ) BAYER PHARM CORP.

XX Taylor I, Pauloski NR, Bigwood D;  
 PI XX  
 DR WPI: 2005-285325/29.

DR XX N-PSDB; AD270356.

PT Providing a patient diagnosis for lung cancer comprises comparing the  
 PT level of expression of genes or gene products in a biological sample from  
 PT the patient with that from a normal individual.

XX Claim 3; SEQ ID NO 42; 60pp; English.

PS The invention relates to providing a patient diagnosis for lung cancer  
 PS comprising comparing the level of expression of genes or gene products in  
 PS a biological sample from the patient with the level of expression of  
 PS genes or gene products in a biological sample from a normal individual.  
 PS Also included are distinguishing between normal and disease tissues,  
 PS monitoring the response of a patient being treated for lung cancer by  
 PS administering an anti-cancer agent, identifying a compound useful for the  
 PS treatment of lung cancer and an array for distinguishing between normal  
 PS and disease tissues (comprising 2 or more probes corresponding to 2 or  
 PS more genes selected from any of the 20 nucleotide sequences given in the  
 PS specification, or 2 or more polypeptides comprising any of the 20 amino  
 PS acid sequences given in the specification). In providing a patient  
 PS diagnosis for lung cancer, one or more genes are selected from any of the  
 PS 200 nucleotide sequences as mentioned in the specification, or one or  
 PS more gene products are polypeptides selected from any of the 20 amino  
 PS acid sequences mentioned in the specification. The methods are useful for  
 PS detecting and treating lung cancer. These may also be used for designing,  
 PS identifying and optimizing therapeutics for cancer. The present sequence  
 PS represents a protein from one of the 200 lung cancer marker genes. Note:

CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX Sequence 269 AA;

Query Match 72.2%; Score 65; DB 9; Length 269;  
 Best Local Similarity 81.2%; Pred. No. 0; 6; Mismatches 3;保守性  
 Matches 13; Indels 0; Gaps 0;  
 QY 1 LVVGLCITCQIKTGAPC 16  
 Db 219 LVVGLCITCQIKTGAPC 234

RESULT 18

ABU04378  
 ID ABU04378 standard; protein; 272 AA.  
 XX  
 AC ABU04378;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1044.  
 DE KW Translational profiling; expressed protein tag; EPT; kinase; Phosphatase;  
 DE receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 DE adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 DE OS Homo sapiens.  
 DE XX WO200278524-A2.

PD 10-OCT-2002.

PP 28-MAR-2002; 2002WO-US009871.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-031001P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCOS INC.

XX PI Chick RM, Tomlinson AJ, Urban RG;  
 DR XX  
 DR WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

PS Example 2; SEQ ID NO 1044; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammalian immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for expressing protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 272 AA;

Query Match 72.2%; Score 65; DB 6; Length 272;  
 Best Local Similarity 81.2%; Pred. No. 0 61; Mismatches 0;  
 Matches 13; Conservative 0; Indels 3; Gaps 0;  
 QY 1 LVVGLCTQIKTGAPC 16  
 Db 222 LVVGLCTQIKTGAPC 237

## RESULT 19

ID ABU04375 standard; protein; 272 AA.  
 XX AC ABU04375;  
 XX DT 29-JAN-2003 (first entry)  
 XX DE Human expressed protein tag (EPT) #1041.

XX KW translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia;  
 OS Homo sapiens.  
 XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX PP 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0324370P.  
 PR 04-DEC-2001; 2001US-0356780P.  
 PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PT Chicz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

XX Example 2; SEQ ID NO 1041; 134pp; English.  
 XX The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immune response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 272 AA;

Query Match 72.2%; Score 65; DB 6; Length 272;  
 Best Local Similarity 81.2%; Pred. No. 0 61; Mismatches 0;  
 Matches 13; Conservative 0; Indels 3; Gaps 0;  
 QY 1 LVVGLCTQIKTGAPC 16  
 Db 222 LVVGLCTQIKTGAPC 237

## RESULT 20

ID ABU04376 standard; protein; 336 AA.  
 XX AC ABU04376;  
 XX DT 29-JAN-2003 (first entry)  
 XX DE Human expressed protein tag (EPT) #1042.

XX KW translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 OS Homo sapiens.  
 XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX PP 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0324370P.  
 PR 04-DEC-2001; 2001US-0356780P.  
 PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.  
 XX PT Chicz RM, Tomlinson AJ, Urban RG;  
 XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

XX Example 2; SEQ ID NO 1042; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immune response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational



CC proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

SQ Sequence 429 AA;

Query Match	72.2%	Score	65	DB	3	Length	429
Best Local Similarity	81.2%	Pred.	No.	0	9	Mismatches	13
Matches		Indels	3	Gaps	0		

Oy 1 LVVGLCTCQIKIGPAC 16  
Db 379 LVVGLCTCQIKIGPAC 394

RESULT 23

ABU03938

ID ABU03938 standard; protein; 429 AA.

XX AC

ABU03938;

XX DT

29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #604.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0295544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0316370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PT Chicz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX DR

New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

XX Example 2; SEQ ID NO 604; 134PP; English.

XX The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and CC polynucleotides are particularly useful for treating or preventing CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for CC treating the above mentioned diseases. This sequence represents an CC expressed protein tag (EPT) isolated from human tissue for translational CC profiling. Note: This sequence does not appear in the printed CC specification but was obtained in electronic format directly from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 429 AA;

Query Match	72.2%	Score	65	DB	6	Length	429
Best Local Similarity	81.2%	Pred.	No.	0	9	Mismatches	13
Matches		Indels	3	Gaps	0		

Oy 1 LVVGLCTCQIKIGPAC 16  
Db 379 LVVGLCTCQIKIGPAC 394

RESULT 24

AAM14001

ID AAM14001 standard; protein; 433 AA.

XX AC AAM14001;

XX DT 23-MAY-1997 (first entry)

XX DE Endopeptidase protein.

XX KW PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE; enolase; radioisotope; antigen.

XX OS Homo sapiens.

XX PN JP08308584-A.

XX RD 26-NOV-1995.

XX PF 19-MAY-1995; 95JP-00145542.

PR 19-MAY-1995; 95JP-00145542.

XX PA (EIKE ) EIKEN KAGAKU KK.

XX DR WPI; 1997-059703/06.

XX PT Introducing tyrosine residues into a protein for radioisotopic labelling

PT - by substitution, addition and/or insertion to a DNA coding for the

PT protein, antigenicity of the protein is unchanged by labelling.

XX PS Disclosure; Page 10-11; 13pp; Japanese.

XX

CC This sequence represents the wild type human enolase (NSE) protein. The

CC primers represented by ATG028-T60285 were used to amplify tyrosine

CC introduced versions of this sequence. The introduced tyrosine residue

CC combine a radioisotope in such a way as to have no substantial effect on

CC the antigenicity of the protein. The peptides with the introduced

CC tyrosine residue are prepared by expressing a recombinant DNA sequence,

CC where the tyrosine residue has been introduced via an insertion or

CC substitution into the wild type sequence. The peptides can then be used

CC in radioimmunoassays, as the introduction of the label does not alter the

CC antigenicity of the protein

SQ Sequence 433 AA;

Query Match

72.2%

Score

65

DB

2

Length

433

Best Local Similarity

81.2%

Pred.

No.

0

9

Mismatches

0

Indels

3

Gaps

0

Oy 1 LVVGLCTCQIKIGPAC 16

**Db** 383 LVVGLCTGQIKTGAPC 398  
**RESULT 25**  
**ID** AAW54357  
**ID** AAW54357 standard; protein; 433 AA.  
**AC** XX  
**AC** AAW54357;  
**XX**  
**DT** 14-AUG-1998 (first entry)  
**XX**  
**DE** Alpha Enolase.  
**XX**  
**KW** Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
**KW** 2D gel electrophoresis; detection.  
**XX**  
**OS** Homo sapiens.  
**XX**  
**PN** WO9810291.A1.  
**XX**  
**PD** 12-MAR-1998.  
**XX**  
**PF** 05-SEP-1997; 97WO-GB002394.  
**XX**  
**PR** 06-SEP-1996; 96GB-00018400.  
**PR** 08-APR-1997; 97GB-00007132.  
**XX**  
**PA** (CLIN-) CENT CLINICAL & BASIC RES.  
**XX**  
**PI** Byrjalsen I, Larsen P, Fey SJ;  
**XX**  
**DR** WPI; 1998-207057/18.  
**XX**  
**PT** Biochemical markers of human endometrium - useful for, e.g. diagnosis of hyperplasia and adenocarcinoma.  
**PT** XX  
**PS** Disclosure; Page 21, 77pp; English.  
**XX**  
**CC** proteins AAW54349-WI4364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis.  
**CC** proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies  
**CC**  
**XX**  
**SQ** Sequence 433 AA;

Query Match 72.2%; Score 65; DB 2; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.9; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 1 LVVGLCTGQIKTGAPC 16  
**Db** 383 LVVGLCTGQIKTGAPC 398

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**RESULT 26**  
**ID** ABU03944  
**ID** ABU03944 standard; protein; 433 AA.  
**AC** XX  
**AC** ABU03944;  
**XX**  
**DT** 29-JAN-2003 (first entry)  
**XX**  
**DB** Human expressed protein tag (EPT) #610.  
**XX**  
**KW** Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
**XX**

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**Db** 383 LVVGLCTGQIKTGAPC 398  
**OS** Homo sapiens.  
**XX**  
**PN** WO200278524-A2.  
**XX**  
**PD** 10-OCT-2002.  
**XX**  
**PF** 28-MAR-2002; 2002WO-US009671.  
**XX**  
**PR** 28-MAR-2001; 2001US-0279495P.  
**PR** 21-MAY-2001; 2001US-029244P.  
**PR** 08-AUG-2001; 2001US-031001P.  
**PR** 01-OCT-2001; 2001US-032670P.  
**PR** 04-DEC-2001; 2001US-033680P.  
**PR** 20-FEB-2002; 2002US-0358985P.  
**XX**  
**PA** (ZYCO-) ZYCOS INC.  
**XX**  
**PI** Chicz RM, Tomlinson AJ, Urban RG;  
**XX**  
**DR** WPI; 2003-040607/03.  
**XX**  
**PT** New polypeptides (e.g. kinases, phosphatases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.  
**XX**  
**PS** Example 2; SEQ ID NO 610; 134pp; English.  
**XX**  
**CC** The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
**XX**  
**SQ** Sequence 433 AA;

Query Match 72.2%; Score 65; DB 6; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.9; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 1 LVVGLCTGQIKTGAPC 16  
**Db** 383 LVVGLCTGQIKTGAPC 398

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**RESULT 27**  
**ID** ABU03942  
**ID** ABU03942 standard; protein; 433 AA.  
**AC** XX  
**AC** ABU03942;  
**XX**  
**DT** 29-JAN-2003 (first entry)  
**XX**  
**DB** Human expressed protein tag (EPT) #608.  
**XX**  
**KW** Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.  
 XX  
 PN WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PR 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 XX  
 PR 21-MAY-2001; 2001US-029254P.  
 XX  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-032670P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCOS INC.  
 XX  
 PT Chicz RM, Tomlinson AJ, Urban RG;  
 DR XX  
 WPI; 2003-040607/03.  
 XX  
 PT New polypeptides (e.g., kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g., colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.  
 XX  
 PS Example 2; SEQ ID NO 608; 134pp; English.

The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

CC sequence 433 AA;

CC Best Local Similarity 81.2%; Score 65; DB 6; Length 433;  
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CC SQ

Query Match 1 LIVGGLCTQKTKGPAC 16  
 Best Local Similarity 81.2%; Score 65; DB 6; Length 433;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 DB 383 LVVGLCTQKTKGPAC 398

RESULT 28  
 ADQ30574  
 ID ADQ30574 standard; protein: 433 AA.  
 AC  
 XX  
 DT 23-SEP-2004 (first entry)  
 DB Pancreas cancer marker - human alpha enolase.  
 XX  
 KW cytostatic; diagnosis'; pancreatic cancer; antibody; antisense construct; differential expression.  
 XX  
 OS Homo sapiens.  
 PN WO2004055519-A2.

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XX  
 PD 01-JUL-2004.  
 XX  
 PR 11-DEC-2003; 2003WO-EP014057.  
 XX  
 PR 17-DEC-2002; 2002EP-00028059.  
 XX  
 PR 05-NOV-2003; 2003EP-00025237.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (SINO-) SINOCENOMAX CO LTD CHINESE NAT HUMAN GEN.  
 XX  
 PT Chen J, Hu L, Liu TH, Liu ZH, Shen Y;  
 XX  
 DR WPI; 2004-48812/L/46.  
 XX  
 PT New specific markers comprises at least one polypeptide up-regulated in pancreatic cancer, useful for diagnosing pancreatic cancer.  
 XX  
 PS Claim 1; SEQ ID NO 61; 381pp; English.

CC The invention relates to a marker (I) for diagnosis of pancreatic cancer comprising at least one polypeptide selected from 55 proteins up-regulated in pancreatic cancer (Table 2 and Table 3, given in the specification) or from 68 proteins with higher levels in pancreatic cancer compared to normal tissue (Table 6, given in the specification).  
 CC (I) is a polypeptide for use as a marker or as a component of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. A compound (antibody, an antibody derivative, an antibody fragment, a peptide, or an antisense construct) identified by screening methods using (I) is useful for treatment or prevention of pancreatic cancer. It is also useful for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. The current polypeptides were found to be differentially expressed in pancreatic tissue obtained from individuals suffering from pancreatic cancer as compared to healthy pancreatic tissue. They have been identified as suitable as markers of pancreatic cancer for early diagnosis of the disease. This sequence corresponds to a protein marker of the invention.

CC Sequence 433 AA;

CC Query Match 1 LIVGGLCTQKTKGPAC 16  
 CC Best Local Similarity 81.2%; Score 65; DB 8; Length 433;  
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CC DB 383 LVVGLCTQKTKGPAC 398

RESULT 29  
 ABB57379  
 ID ABB57379 standard; protein: 434 AA.  
 AC  
 XX  
 DT 07-AUG-2003 (revised)  
 DT 08-MAR-2002 (first entry)  
 DB Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 10.  
 XX  
 KW Rat; heart; cardiot; myocardial necrosis; cardiac hypertrophy;  
 KW cardiac insufficiency.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN WO200183705-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PR 27-APR-2001; 2001WO-JP003700.  
 XX  
 PR 27-APR-2000; 2000JP-00126741.

XX  
PA (KYOW ) KYOWA HAKKO KOCYO KK.  
XX  
PT Yamada Y, Sekine S, Kikuchi Y, Sakurada K;  
XX  
DR WPI; 2002-075160/10.  
DR N-PSDB; AB199919.

PS  
XK  
PT  
PT  
PT  
XX

Genes having differential expression in fetal and adult heart tissue useful for screening potential drugs for promoting repair of damage caused by myocardial necrosis.

XX  
Claim 53; Page 98-100; 171P; Japanese.

CC The invention relates to gene sequences (ABI199915-ABI199934) having modified expression in fetal heart tissue as compared to adult heart tissue and the encoded proteins (ABB57375-ABB57392). The genes have CC cardiac activity and may be useful for the promotion of the repair of damage to heart tissue caused by myocardial necrosis. The gene sequences are useful for screening potential compounds for the ability to influence disease associated with myocardial necrosis. Drugs identified by the screening methods may be used to treat and prevent disease with which myocardial necrosis is associated, such as cardiac hypertrophy and cardiac insufficiency. Diagnosis of diseases such as those above is also disclosed. (Updated on 07-AUG-2003 to correct OS field.)

SQ  
XX  
Sequence 434 AA;

Query Match 72.2%; Score 65; DB 5; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.91;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTCQIKTGpac 16  
Db 384 LVVGLCTCQIKTGpac 399

RESULT 30

ABP65147  
ID ABP65147 standard; protein: 434 AA.

XX  
AC ABP65147;

XX  
DT 12-NOV-2002 (first entry)

XX  
DE Hypoxia-regulated protein #21.

XX  
KW Cytotoxic; vasoconstrictor; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neovascular stress; preeclampsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200246465-A2.

XX  
PD 13-JUN-2002.

XX  
PP 10-DEC-2001; 2001WO-GB005558.

XX  
PR 08-DEC-2000; 2000GB-00030076.

PR 08-FEB-2001; 2001GB-0003156.

PR 25-OCT-2001; 2001GB-00025666.

XX  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
XX  
White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
XX  
DR WPI; 2002-627239/67.

PR Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially regulated gene.

XX  
PS  
XK  
Claim 35; Page 344; 538pp; English.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV7816 and ABP65061-ABP6525 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss

XX  
Sequence 434 AA;

Query Match 72.2%; Score 65; DB 5; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.91;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTCQIKTGpac 16  
Db 384 LVVGLCTCQIKTGpac 399

Search completed: April 3, 2006, 08:04:17  
Job time : 85 Secs

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GenCore version 5.1.7

### OM protein - protein search, using SW model.

Run on:

April 3, 2006, 08:03:01 ; Search time 15 Seconds

(without alignments) 102.631 Million cell updates/sec

Title: US-09-647-457F-3

Perfect score: 90

Sequence: 1 LVVGLCTCQIKTGPMC 16

Scoring table: BL050m62

Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 100 summaries

Database : PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	74	82.2	458	2 I37360 phosphopyruvate hy
2	65	72.2	395	2 I50026 phosphopyruvate hy
3	65	72.2	433	1 A37210 phosphopyruvate hy
4	65	72.2	434	1 NORUG phosphopyruvate hy
5	65	72.2	434	1 NOMSB phosphopyruvate hy
6	65	72.2	434	1 NOXL phosphopyruvate hy
7	65	72.2	434	1 JC039 hypothetical prote
8	65	72.2	434	2 JC186 phosphopyruvate hy
9	65	72.2	434	2 JC187 phosphopyruvate hy
10	65	72.2	434	2 JC0756 phosphopyruvate hy
11	65	72.2	434	2 S1.0246 phosphopyruvate hy
12	65	72.2	434	2 S1.0247 phosphopyruvate hy
13	65	72.2	434	2 S02072 phosphopyruvate hy
14	65	72.2	434	2 A29170 phosphopyruvate hy
15	65	72.2	434	2 A32132 phosphopyruvate hy
16	65	72.2	434	2 A2742 phosphopyruvate hy
17	65	72.2	434	2 A32126 phosphopyruvate hy
18	56	62.2	434	2 T25040 phosphopyruvate hy
19	55	61.1	433	2 S07586 phosphopyruvate hy
20	55	61.1	433	2 A32850 phosphopyruvate hy
21	53	58.9	431	2 A53665 phosphopyruvate hy
22	52	57.8	446	2 T0267 phosphopyruvate hy
23	51	56.7	326	2 JQ1186 phosphopyruvate hy
24	51	56.7	444	2 JQ1185 phosphopyruvate hy
25	51	56.7	444	2 JQ1187 phosphopyruvate hy
26	51	56.7	446	2 T02221 phosphopyruvate hy
27	50	55.6	445	2 S39203 phosphopyruvate hy
28	49	54.4	2 446	2 T12341 phosphopyruvate hy
29	49	54.4	2 446	2 S16257 phosphopyruvate hy
30	48	53.3	372	2 S24996 phosphopyruvate hy
31	47.5	52.8	1620	2 T27283 phosphopyruvate hy
32	47.5	52.8	2946	2 T15840 phosphopyruvate hy
33	47	52.2	446	2 S42206 phosphopyruvate hy
34	46.5	51.7	437	1 NOBY phosphopyruvate hy
35	46.5	51.7	437	1 NOBY phosphopyruvate hy
36	46	51.1	125	1 VSM7A2 alpha-2-thionin -
37	46	51.1	137	2 S07648 thionin precursor,
38	46	51.1	477	2 A98768 protein endopeptidase F2
39	45	50.0	329	2 AH3559 thioredoxin [imp]
40	44	48.9	43	2 S13581 collagen alpha 1(I)
41	44	48.9	959	2 S18892 MSH1 protein - Yea
42	43	47.8	85	2 E70531 phosphopyruvate hy
43	43	47.8	456	2 S77562 soluble vascular e
44	43	47.8	1006	2 T00050 hypothetical prote
45	43	47.8	1338	2 S05982 hypothetical prote
46	43	47.8	1331	2 T22769 hypothetical prote
47	42	46.7	142	2 A71097 phosphopyruvate hy
48	42	46.7	497	2 AG3134 phosphopyruvate hy
49	42	46.7	231	2 D64486 hypothetical prote
50	42	46.7	261	2 A53191 thionin precursor,
51	42	46.7	261	2 S33356 hypothetical prote
52	42	46.7	345	2 A05279 surface antigen 51
53	42	46.7	429	2 H83191 betacellulin precu
54	42	46.7	497	2 E88087 N-ethyl-lammelina ch
55	42	46.7	498	2 E99153 genome polypeptide ch
56	41	45.6	3175	1 RRREVW hypothetical prote
57	41	45.6	335	2 T2880 hypothetical protein
58	41	45.6	137	2 S22515 GLP1 protein precu
59	41	45.6	177	2 A37408 notch-1 protein -
60	41	45.6	178	2 JC1467 notch protein homo
61	41	45.6	585	2 E88087 protein B054.6 [1]
62	40.5	45.6	3106	1 S33868 laminin alpha-2 ch
63	40.5	45.0	2 T8906 hypothetical protein	
64	40.5	45.0	1295	2 A32901 hypothetical protein
65	40.5	45.0	2531	2 S18188 notch-1 protein homo
66	40.5	45.0	2555	2 A46019 probable thiamin b
67	40.5	45.0	3106	1 S33868 phosphopyruvate hy
68	40	44.4	132	2 T0463 probable thiamin b
69	40	44.4	277	2 C92571 probable thiamin b
70	40	44.4	314	2 R86532 probable thiamin b
71	40	44.4	314	2 F72090 probable thiamin b
72	40	44.4	433	2 H70141 phosphopyruvate hy
73	40	44.4	440	2 T32190 phosphopyruvate hy
74	40	44.4	574	2 T34208 phosphopyruvate hy
75	40	44.4	3672	2 T23433 phosphopyruvate hy
76	40	44.4	3704	2 T37316 phosphopyruvate hy
77	39.5	43.9	372	2 T29359 phosphopyruvate hy
78	39.5	43.9	490	2 S93113 phosphopyruvate hy
79	39.5	43.9	772	2 S32269 phosphopyruvate hy
80	39.5	43.9	2524	2 A35844 phosphopyruvate hy
81	39	43.3	139	2 T23371 phosphopyruvate hy
82	39	43.3	220	2 T31184 phosphopyruvate hy
83	39	43.3	293	2 T49564 phosphopyruvate hy
84	39	43.3	314	2 T27686 phosphopyruvate hy
85	39	43.3	364	2 G86180 phosphopyruvate hy
86	39	43.3	374	2 T20110 phosphopyruvate hy
87	39	43.3	513	2 A24309 phosphopyruvate hy
88	39	43.3	522	1 GHWVR1 phosphopyruvate hy
89	39	43.3	665	2 T88979 phosphopyruvate hy
90	39	43.3	689	2 TS2060 phosphopyruvate hy
91	39	43.3	992	1 GHWVR3 phosphopyruvate hy
92	39	43.3	1063	1 GHWVR7 phosphopyruvate hy
93	39	43.3	1063	1 GHWVR4 phosphopyruvate hy
94	39	43.3	1063	1 GHWVR phosphopyruvate hy
95	39	43.3	1239	1 VERNE phosphopyruvate hy
96	39	43.3	1240	1 VERNE phosphopyruvate hy
97	39	43.3	1241	2 S26373 phosphopyruvate hy
98	39	43.3	1242	2 A56605 phosphopyruvate hy
99	39	43.3	1242	2 S72350 phosphopyruvate hy
100	39	43.3	1246	2 T46612 phosphopyruvate hy

## ALIGNMENTS

RESULT 1  
 137360 phosphopyruvate hydratase (EC 4.2.1.11), lung - human  
 N;Alternate names: enolase  
 C;Species: Homo sapiens (man)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C;Accession: I37360; S22071  
 A;Reference number: A37210; MUID:91113295; PMID:2275753  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-433 <CHI>  
 A;Cross-references: UNIPROT:P25704; UNIPARC:UP1000017606F  
 C;Superfamily: enolase  
 C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase  
 F;1/Modified site: acetylated amino end (Ala) #status: experimental  
 A;Note: submitted to the EMBL Data Library, June 1992  
 A;Accession: I37360  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Residues: 1-458 <VER>  
 A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphopyruvate  
 A;Pathway: gluconeogenesis; glycolysis  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
 F;219;364/Active site: Glu; Lys #status predicted  
 F;254;308;336/Binding site: magnesium 2 (Ser) #status predicted  
 Query Match 82.2%; Score 74; DB 2; Length 433;  
 Best Local Similarity 87.5%; Pred. No. 0.0059;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LVVGLCCTQIKTGPC 16  
 Db 407 LVVGLCCTQIKTGPTC 422  
 RESULT 2  
 150026 phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)  
 N;Alternate names: alpha-enolase  
 C;Species: Alligator mississippiensis (American alligator)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
 C;Accession: I50026  
 A;Title: Molecular evidence for the origin of birds.  
 A;Reference number: A53470; MUID:94195794; PMID:8146164  
 A;Accession: I50026  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown; translate  
 A;Molecule type: mRNA  
 A;Residues: 1-395 <HED>  
 A;Cross-references: UNIPROT:P42897; UNIPARC:UPI0000129F57; GB:I28078; NID:9472796; PIDN:  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; hydro-lyase  
 Query Match 72.2%; Score 65; DB 2; Length 395;  
 Best Local Similarity 81.2%; Pred. No. 0.013; Mismatches 13; Conservative 0; Indels 0; Gaps 0;  
 QY 1 LVVGLCCTQIKTGPC 16  
 Db 362 LVVGLCCTQIKTGPTC 377  
 RESULT 3  
 A7210 phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit  
 N;Alternate names: enolase beta  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 05-Oct-2004  
 C;Accession: A37210  
 J. Protein Chem. 9, 427-432, 1990  
 A;Title: The primary structure of rabbit muscle enolase.  
 A;Reference number: A37210; MUID:91113295; PMID:2275753  
 A;Accession: I37210  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-433 <CHI>  
 A;Cross-references: UNIPROT:P25704; UNIPARC:UP1000017606F  
 C;Superfamily: enolase  
 C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase  
 F;1/Modified site: acetylated amino end (Ala) #status: experimental  
 Query Match 72.2%; Score 65; DB 2; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.014; Mismatches 13; Conservative 0; Indels 0; Gaps 0;  
 Matches 13; Gaps 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCCTQIKTGPC 16  
 Db 383 LVVGLCCTQIKTGAPC 398  
 RESULT 4  
 N0HUG phosphopyruvate hydratase (EC 4.2.1.11) gamma - human  
 N;Alternate names: enolase gamma; neuron-specific enolase  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 05-Oct-2004  
 C;Accession: JU0060; S16363; S02077; I52569; S02616; S28303  
 R;Oliva, D.; Barba, G.; Barbieri, G.; Giallongo, A.; Reo, S.  
 Gene 79, 355-360, 1989  
 A;Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.  
 A;Reference number: JU0060; MUID:90006764; PMID:2792767  
 A;Accession: JU0060  
 A;Molecule type: mRNA  
 A;Residues: 1-334 <OIL>  
 A;Cross-references: UNIPROT:PO9104; UNIPARC:UPI000013CBFL; GB:M22349; NID:951199; PIDN:  
 R;Oliva, D.; Cali, L.; Reo, S.; Giallongo, A.  
 Genomics 10, 157-165, 1991  
 A;Title: Complete structure of the human gene encoding neuron-specific enolase.  
 A;Reference number: S16163; MUID:91257823; PMID:2045099  
 A;Accession: S16163  
 A;Molecule type: DNA  
 A;Residues: 1-334 <OIL>  
 A;Cross-references: UNIPARC:UPI000013CBFL; GB:Xc1956; NID:931164; PIDN:CAA36215.1; PID:  
 R;McLeese, S.M.; Dunbar, B.; Foothergill, J.E.; Hinks, L.J.; Day, I.N.M.  
 Eur. J. Biochem. 178, 413-417, 1988  
 A;Title: Complete amino acid sequence of the neurone-specific gamma isozyme of enolase  
 A;Reference number: S02077; MUID:89091176; PMID:3208766  
 A;Accession: S02077  
 A;Molecule type: mRNA  
 A;Residues: 2-33, 'Q', 5-239, 'W', 241-434 <MCA>  
 A;Cross-references: UNIPARC:UPI000015TB77; EMBL:X13120; NID:931145; PIDN:CAA31512.1; PID:  
 A;Note: part of this sequence was confirmed by protein sequencing  
 A;Note: 264-Ala and 395-Ala were also found  
 R;Van Obberghen, E.; Kamholz, J.; Bishop, J.G.  
 J. Neurosci. Res. 19, 450-456, 1988  
 A;Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tum  
 A;Reference number: I56569; MUID:8825928; PMID:3385803  
 A;Accession: I56569  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 'GC', 29-125, 'N', 128-434 <VAN>  
 A;Cross-references: UNIPARC:UPI000016A897; GB:M36768; NID:9182117; PIDN:AAA52388.1; PID:  
 R;Day, I.N.M.; Alsop, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.  
 FEBS Lett. 222, 139-143, 1987  
 A;Title: Sequence conservation in the 3'-untranslated regions of neurone-specific enolases  
 A;Reference number: S02616; MUID:88005129; PMID:3653393  
 A;Cross-references: UNIPARC:UPI0000172FAB; GB:Y00691; GB:M27610  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 425-434 <DAY>  
 A;Cross-references: UNIPARC:UPI0000172FAB; GB:Y00691; GB:M27610

R;Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wischik, C.M.  
Biochim. Biophys. Acta 1158, 120-128, 1993  
A;Title: Characterization of an epitope specific to the neuron-specific isoform of human  
of beta/A4-protein.  
A;Reference number: S38303; MUID:94002176; PMID:7691181  
A;Accession: S38303  
A;Molecule type: protein  
A;Residues: 156-173 <HAR>  
A;Cross-references: UNIPARC:UPI0000172PAC  
C;Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in mamma  
C;Genetics: Thr-191 may be important for the enhanced tolerance to chloride ions of neur  
C;Function:  
A;Gene: GDB:ENO2  
A;Cross-references: GDB:119872; OMIM:131360  
A;Map position: 12p13-12p13  
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2  
C;Complex: homodimer  
C;Function:  
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos  
A;Pathway: gluconeogenesis; glycolysis  
C;Superfamily: enolase  
C;Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;  
F;2-424/product: phosphopyruvate hydratase gamma #status predicted <MAP>  
F;2/Modified site: blocked amino end (Ser)  
F;4/Binding site: magnesium 2 (Ser) #status predicted  
F;210,343/Active site: Glu, Lys #status predicted  
F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted  
Query Match 72.2%; Score 65; DB 1; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LVVGLCTQIKTGpac 16  
Db 384 LVVGLCTQIKTGpac 399

RESULT 5  
NOMSB  
phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse  
N;Alternate name: enolase beta  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-Oct-2004  
C;Accession: S17109; S18036; S29675; A33221  
R;Lamande, N.; Broset, A.; Keller, A.; Lucas, M.; Lazar, M.  
submitted to the EMBL Data Library, September 1991  
A;Reference number: S17109  
A;Accession: S17109  
A;Molecule type: DNA  
A;Residues: 1-34 <LM>  
A;Cross-references: UNIPROT:P21550; UNIPARC:UPI000001937; EMBL:X61600; NID:950848; PIDN  
R;Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.  
submitted to the EMBL Data Library, October 1991  
A;Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th  
A;Reference number: S18036  
A;Accession: S18036  
A;Molecule type: mRNA  
A;Residues: 1-34 <PT>  
A;Cross-references: UNIPARC:UPI000001937; EMBL:X62667; NID:950143; PIDN:CAA44540.1; PID  
R;Lazar, M.; Lamande, N.; Broset, S.; Lucas, M.; Keller, A.  
submitted to the EMBL Data Library, February 1991  
A;Residue number: S29675  
A;Accession: S29675  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-434 <LMZ>  
A;Cross-references: UNIPARC:UPI000001937; EMBL:X57747; NID:950846; PIDN:CAA40913.1; PID  
R;Lamande, N.; Mazo, A.M.; Lucas, M.; Montaraz, D.; Pinset, C.; Gros, F.; Legault-Demar  
Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989  
A;Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre  
A;Reference number: A33921; MUID:89282789; PMID:2734297  
A;Accession: A33921  
A;Status: preliminary

RESULT 6  
NOXL  
phosphopyruvate hydratase (EC 4.2.1.11) ENOL - African clawed frog  
N;Alternate name: enolase ENOL  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 05-Oct-2004  
C;Accession: S00463  
R;Segil, N.; Shrutiowski, A.; Dworkin, M.B.; Dworkin-Rastl, E.  
Biochem. J. 251, 31-39, 1988  
A;Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterization  
A;Reference number: S00463; MUID:88268812; PMID:3390159  
A;Accession: S00463  
A;Molecule type: mRNA  
A;Residues: 1-34 <SEG>  
A;Cross-references: UNIPROT:P08734; UNIPARC:UPI000171530; EMBL:Y00718; NID:964679; PID  
C;Genetics:  
A;Gene: ENOL  
C;Function:  
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos  
A;Pathway: gluconeogenesis; glycolysis  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; magn  
F;4/Binding site: magnesium 2 (Ser) #status predicted  
F;210,343/Active site: Glu, Lys #status predicted  
F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted  
Query Match 72.2%; Score 65; DB 1; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LVVGLCTQIKTGpac 16  
Db 384 LVVGLCTQIKTGpac 399

RESULT 7  
JCL039  
phosphopyruvate hydratase (EC 4.2.1.11) - rat  
N;Alternate names: neuron-specific enolase  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Mar-1993 #sequence\_revision 19-Oct-1995 #text\_change 03-May-1996  
C;Accession: JCL039  
R;Zhao, C.; Wang, L.B.; Song, X.W.; Zhang, J.Y.  
Chinese Biochem. J. 10, 270-273, 1994  
A;Title: cDNA cloning and sequencing of the NSE gene from rat brain.  
A;Reference number: JCL039  
A;Accession: JCL039  
A;Molecule type: mRNA  
A;Residues: 1-434 <ZHA>

A;Cross-references: UNIPARC:UPI000017606E  
 A;Experimental source: brain, Wistar  
 C;Comment: This enzyme is a specific marker protein for the development of nervous system  
 C;Genetics: use  
 C;Superfamily: enolase  
 C;Keywords: brain; carbon-oxygen lyase; hydro-lyase

**RESULT 8**

JC4186 phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken Score 65; DB 2; Length 434; Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

N;Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase  
 C;Species: Gallus gallus (chicken)  
 C;Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
 C;Accession: JC4186  
 R;Tanka, M.; Maeda, K.; Nakashima, K.  
 J;Bloch, M., 197, 554-559, 1995  
 A;Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: phosphoprotein predicted  
 A;Reference number: JC4186; MUID:9355305; PMID:7629021  
 A;Molecule type: mRNA  
 A;Residues: 1-134 <TAN>  
 A;Cross-references: UNIPROT:P51913; UNIPARC:UPI0000171311; DDBJ:D37900; NID:9974175; PIR:  
 A;Experimental source: brain  
 C;Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein  
 F;4;Binding site: phosphate (Tyr); (covalent) #status predicted

Query Match 72.2%; Score 65; DB 2; Length 434; Best Local Similarity 81.2%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

**RESULT 9**

JC4187 phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken Score 65; DB 2; Length 434; Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

N;Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase  
 C;Species: Gallus gallus (chicken)  
 C;Date: 14-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
 C;Accession: JC4187  
 R;Tanka, M.; Maeda, K.; Nakashima, K.  
 J;Bloch, M., 197, 554-559, 1995  
 A;Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: phosphoprotein predicted  
 A;Reference number: JC4186; MUID:9355305; PMID:7629021  
 A;Molecule type: mRNA  
 A;Residues: 1-434 <TAN>  
 A;Cross-references: UNIPROT:P51913; EMBL:X51957; NID:934788; PID:CAN36216-1; PIR:  
 R;Giallongo, A.; Venturolla, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.  
 J;Bloch, M., 214, 367-374, 1993  
 A;Title: Structural features of the human gene for muscle-specific enolase. Differential  
 A;Reference number: S33330; MUID:93292497; PMID:8515787  
 A;Molecule type: DNA  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Accession: S33330  
 A;Cross-references: UNIPARC:UPI00016A894; EMBL:X56932; NID:931166; PID:CAM40163-1; PI:  
 A;Gene: GDB:EN03  
 A;Cross-references: GDB:119873; OMIM:131370  
 A;Map position: 1Pter-1P12  
 A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skeletal  
 C;Genetics: use  
 C;Keywords: activated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein  
 F;1;Modified site: acetylated amino end (Met) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 434; Best Local Similarity 81.2%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

**RESULT 10**

S06756 phosphopyruvate hydratase (EC 4.2.1.11) beta - human Score 65; DB 2; Length 434; Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

N;Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, muscle  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
 C;Accession: S06756; S14759; S15933; S33330; S08685; S31650  
 R;Peshavarria, M.; Hinks, L.J.; Day, I.N.M.  
 Nucleic Acids Res. 17, 8862, 1989  
 A;Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic  
 A;Accession: S06756  
 A;Molecule type: mRNA  
 A;Residues: 1-434 <PSS>  
 A;Cross-references: UNIPROT:P13929; UNIPARC:UPI00016A896; EMBL:X16504; NID:931169; PID:  
 R;Peshavarria, M.; Day, I.N.M.  
 J;Bloch, M., 275, 427-433, 1991  
 A;Title: Molecular structure of the human muscle-specific enolase gene (ENO3).  
 A;Reference number: S14759; MUID:9122137; PMID:1840492  
 A;Status: nucleic acid sequence not shown  
 A;Accession: S14759  
 A;Molecule type: DNA  
 A;Residues: 1-434 <PSS>  
 A;Cross-references: UNIPARC:UPI00016A896; EMBL:X55976  
 R;Cali, L.; Feo, S.; Oliva, D.; Giallongo, A.  
 Nucleic Acids Res. 18, 1893, 1990  
 A;Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE)  
 A;Reference number: S15933; MUID:9024587; PMID:2336366  
 A;Accession: S15933  
 A;Molecule type: mRNA  
 A;Residues: 1-84, 'A', 86-161, 'K', 163-434 <CAL>  
 A;Cross-references: UNIPARC:UPI000161026; EMBL:X51957; NID:934788; PID:CAN36216-1; PIR:  
 R;Giallongo, A.; Venturolla, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.  
 A;Title: Structural features of the human gene for muscle-specific enolase. Differential  
 A;Reference number: S33330; MUID:93292497; PMID:8515787  
 A;Molecule type: DNA  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Accession: S33330  
 A;Cross-references: UNIPARC:UPI00016A894; EMBL:X56932; NID:931166; PID:CAM40163-1; PI:  
 A;Gene: GDB:EN03  
 A;Cross-references: GDB:119873; OMIM:131370  
 A;Map position: 1Pter-1P12  
 A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skeletal  
 C;Genetics: use  
 C;Keywords: activated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein  
 F;1;Modified site: acetylated amino end (Met) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 434; Best Local Similarity 81.2%; Pred. No. 0.014; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

**RESULT 11**

S10246 phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse Score 65; DB 2; Length 434; Qy 1 LVVGLCTQIKTGpac 16 Db 384 LVVGLCTQIKTGpac 399

N;Alternate names: 2-phosphoglycerate dehydratase; enolase alpha  
 C;Species: Mus musculus (house mouse)  
 C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C;Accession: S10246; A56781  
 R;Raghav, M.; Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C  
 Nucleic Acids Res. 18, 3658, 1990

A;Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.  
A;Reference number: S10246; MUID:90301487; PMID:2362815  
A;Accession: S10246  
A;Molecule type: mRNA  
A;Residues: I-434 <KOG>  
A;Cross-references: UNIPROT:PI7182; UNIPARC:UPI000161F48; EMBL:X52379; NID:955490; PIDN  
R;Botalico, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.  
Arterioscler, Thromb, 13, 264-275, 1993  
A;Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with ch  
soform.  
A;Reference number: A56781; MUID:93152553; PMID:8427861  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 'X', '60, 'X', '62-67, 'X', '69-71, 'XX', '100-109, 'X', '111-112, 'X', '114, 'X', '184-185, 'X'  
A;Cross-references: UNIPARC:UPI000176064; UNIPARC:UPI000176065; UNIPARC:UPI000176066;  
A;Experimental source: peritoneal macrophages  
A;Note: sequence modified after extraction from NCBI backbone  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Best Local Similarity 81.2%; Pred. No. 0.014; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAPC 16  
Db 384 LVVGLCTCQIKTGAPC 399

RESULT 12

S10247 phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse  
N;Alternate names: 2-phosphoglycerate dehydratase; enolase gamma  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: S10247  
R;Khaghad, M.; Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C  
Nucleic Acids Res. 18, 3638, 1990  
A;Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.  
A;Reference number: S10246; MUID:90301487; PMID:2362815  
A;Accession: S10247  
A;Molecule type: mRNA  
A;Residues: 1-434 <KOG>  
A;Cross-references: UNIPROT:PI7183; UNIPARC:UPI000001520; EMBL:X52380; NID:955494; PIDN  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAPC 16  
Db 384 LVVGLCTCQIKTGAPC 399

RESULT 14

A29170 phosphopyruvate hydratase (EC 4.2.1.11) alpha - human  
N;Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
C;Accession: S11696; A29170; S52858; A31183  
R;Giallongo, A.; Oliva, D.; Cali, L.; Barba, G.; Barbieri, G.; Feo, S.  
A;Title: Structure of the human gene for alpha-enolase.  
A;Reference number: S11696; MUID:90323004; PMID:2373081  
A;Accession: S11696  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-434 <GT>  
A;Cross-references: UNIPROT:PO6733; UNIPARC:UPI00013C9AF; EMBL:X16288; NID:931172; PI  
R;Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Shone, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986  
A;Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alp  
A;Reference number: A29170; MUID:86313654; PMID:3529090  
A;Accession: A29170  
A;Molecule type: mRNA  
A;Residues: 1-434 <GT>  
A;Cross-references: UNIPARC:UPI00013C9AF; GB:MA4328; NID:9182113; PIDN:AMAS52387.1; PI  
A;Note: the authors translated the codon AAG for residue 193 as His  
R;Walter, M.; Leidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northemann, W.  
submitted to the EMBL Data Library, February 1995  
A;Description: Auto-reactive epitopes within the human alpha-enolase and their recogniti  
A;Reference number: S52858  
A;Accession: S52858  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-251, S', 253-434 <WAL>  
A;Cross-references: UNIPARC:UPI00016A207; EMBL:X84907; NID:9693932; PIDN:CAA59331.1; E  
A;Experimental source: endometrial carcinoma cell line HECA-1B  
R;Miles, L.A.; Dahlberg, C.M.; Plescia, J.; Pelez, J.; Kato, K.; Plow, E.P.  
Biochemistry 30, 1682-1691, 1991  
A;Title: Role of cell-surface lysines in plasminogen binding to cells: identification c  
A;Reference number: A39183; MUID:9129243; PMID:1847072  
A;Accession: A39183  
A;Molecule type: protein  
A;Residues: 170-182, I, 184, 'R', 186-190, 245-252 <ML>  
A;Cross-references: UNIPARC:UPI000176068; UNIPARC:UPI000176059  
A;Gene: GDB:ENOL  
A;Genetic: C;Genetics:  
A;Cross-references: GDB:119871; OMIM:172430  
A;Map position: 1p36-1p36  
A;Intron: 29/1; 67/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
C;Function:  
A;Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosphogl  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
F;2-434/Product: phosphopyruvate hydratase alpha #Status predicted <MMT>  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAPC 16  
Db 384 LVVGLCTCQIKTGAPC 399

Db 384 LVVGLCTGQIKTGAPC 399  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
 C;Superfamily: enolase  
 A;Residues: 1-434 <WIS>  
 A;Cross-references: UNIPROT:P19140; UNIPARC:UPI0001711A5; GB:X14195; NID:962455; PIDN:  
 C;Keywords: Carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
 C;Superfamily: enolase  
 A;Residues: 1-434 <SAK>  
 A;Cross-references: UNIPROT:P04764; UNIPARC:UPI00015C86D; GB:X02610; NID:956106; PIDN:  
 C;Species: Anas platyrhynchos (domestic duck)  
 C;Accession: A32132  
 R;Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.; E.J. Cell Biol. 107, 2729-2736, 1988  
 A;Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens structure  
 A;Reference number: A92750; MUID:89079778; PMID:2462567  
 A;Molecule type: mRNA  
 A;Residues: 1-434 <WIS>  
 A;Cross-references: UNIPROT:P19140; UNIPARC:UPI0001711A5; GB:X14195; NID:962455; PIDN:  
 C;Keywords: Carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
 Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014; DB 2; Length 434;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 Db 384 LVVGLCTGQIKTGAPC 399  
 RESULT 16  
 A24742 phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat  
 N;Alternate names: 2-phosphoglycerate dehydratase; enolase gamma; neuronal enolase  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 05-Oct-2004  
 C;Accession: A24742; PIDN: P0006  
 R;Sakimura, K.; Kubuya, E.; Obinata, M.; Odani, S.; Takahashi, Y.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7452-7457, 1985  
 A;Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific enolase  
 A;Reference number: A24742; MUID:86042683; PMID:2865729  
 A;Accession: A24742  
 A;Molecule type: mRNA  
 A;Residues: 1-434 <SAK>  
 A;Cross-references: UNIPROT:P07323; UNIPARC:UPI0001684CA; GB:M11931; NID:9204041; PIDN:  
 R;Sakimura, K.; Kubuya, E.; Takahashi, Y.; Suzuki, Y.  
 Gene 60, 103-113, 1987  
 A;Title: The structure and expression of neuron-specific enolase gene.  
 A;Reference number: P0006; MUID:8152493; PMID:2450052  
 A;Accession: P0006  
 A;Molecule type: DNA  
 A;Residues: 1-28 <SA2>  
 A;Cross-references: UNIPROT:UPI00014B62B; GB:M22770; GB:M18742; NID:9205766; PIDN:AAA41  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
 Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014; DB 2; Length 434;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 Db 384 LVVGLCTGQIKTGAPC 399  
 RESULT 17  
 A23126 phosphopyruvate hydratase (EC 4.2.1.11) alpha - rat  
 N;Alternate names: enolase alpha; nonneuronal enolase  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 05-Oct-2004  
 C;Accession: A23126  
 R;Sakimura, K.; Kubuya, E.; Obinata, M.; Takahashi, Y.  
 • • •  
 RESULT 18  
 T25040 hypothetical protein T21B10.2 - Caenorhabditis elegans  
 N;Alternate names: 2-phosphoglycerate dehydratase; enolase gamma; neuronal enolase  
 C;Species: Caenorhabditis elegans  
 C;Accession: T25040  
 R;Baynes, C.  
 submitted to the EMBL Data Library, December 1995  
 A;Reference number: 219973  
 A;Accession: T25040  
 A;Status: Preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-34 <WIL>  
 A;Cross-references: UNIPROT:Q27527; UNIPARC:UPI000164061; EMBL:Z68318; PIDN:CAA92692.1  
 A;Experimental source: clone T21B10  
 C;Genetics:  
 A;Gene: CESP:T21B10.2  
 A;Map position: 2  
 A;Introns: 29/1; 344/3  
 C;Superfamily: enolase  
 Query Match 62.2%; Score 56; DB 2; Length 434;  
 Best Local Similarity 75.0%; Pred. No. 0.35; DB 2; Length 434;  
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 Db 385 LVVGLATGQIKTGAPC 400  
 RESULT 19  
 S07586 phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly (Drosophila melanogaster)  
 N;Alternate names: enolase  
 C;Species: Drosophila melanogaster  
 C;Accession: S07586  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 R;Bishop, J.G.; Corces, V.G.  
 Nucleic Acids Res. 18, 191, 1990  
 A;Title: The nucleotide sequence of a Drosophila melanogaster enolase gene.  
 A;Reference number: S07586; MUID:90174924; PMID:2106662  
 A;Accession: S07586  
 A;Molecule type: DNA  
 A;Residues: 1-433 <BIS>  
 A;Cross-references: UNIPROT:P15007; UNIPARC:UPI000129F6C; EMBL:X17034; NID:97945; PIDN:  
 C;Genetics:  
 A;Gene: FlyBase:Eco  
 A;Cross-references: FlyBase:FBgn0000579  
 A;Map position: 22A  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
 Query Match 61.1%; Score 55; DB 2; Length 433;  
 Best Local Similarity 75.0%; Pred. No. 0.49;



A;Accession: JQ1185  
A;Molecule type: mRNA  
A;Residues: 1-444 <VAN>  
A;Cross-references: UNIPROT:P26300; UNIPARC:UPI000129F76; EMBL:X58108; NID:919280; PIDN  
A;Experimental source: cv. Orlando  
C;Comment: Introns in the coding regions for residues 1-110 and 437-444 are not revealed  
C;Genetics:  
A;Introns: 110/3; 137/3; 171/3; 198/3; 223/3; 244/3; 270/3; 335/3; 352/3; 382/2; 399/3;  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 56.7%; Score 51; DB 2; Length 444;  
Best Local Similarity 68.8%; Pred. No. 2.1; Mismatches 0; Indels 5; Gaps 0;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 393 LAVGLSTGQIKTGAPC 16  
Db 393 LAVGLSTGQIKTGAPC 408

RESULT 25

JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - *Arabidopsis thaliana*  
N;Alternate names: enolase  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: JQ1187; F84781  
R;Van Der Straeten, D.; Rodrigues-Pousada, R.A.; Goodman, H.M.; Van Montagu, M.  
Plant Cell 3, 719-735, 1991  
A;Title: Plant enolase: gene structure, expression, and evolution.  
A;Reference number: JQ1185; MUID:93044507; PMID:1841726  
A;Molecule type: DNA  
A;Residues: 1-444 <VAN>  
A;Cross-references: UNIPROT:P25695; UNIPARC:UPI000000D31; EMBL:X8107; NID:916270; PIDN  
R;Linn, X.; Kahl, S.; Ronksley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Stren, M.; Vanaken, S.E.; Umayam, L.; Talon, L.;  
eubs, D.; Nieman, W.C.; White, O.; Esen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: F84781  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-444 <STO>  
A;Cross-references: UNIPARC:UPI000000D31; GB:AB002093; NID:94581151; PIDN:AAD24635; 1; G  
C;Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phospho  
C;Genetics:  
A;Gene: At2g36530  
A;Map position: 2  
A;Introns: 22/3; 65/3; 81/3; 110/3; 137/3; 198/3; 244/3; 270/3; 335/3; 399/3; 418/3  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 56.7%; Score 51; DB 2; Length 444;  
Best Local Similarity 68.8%; Pred. No. 2.1; Mismatches 0; Indels 5; Gaps 0;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 393 LAVGLSTGQIKTGAPC 16  
Db 393 LAVGLSTGQIKTGAPC 408

RESULT 26

T02221 phosphopyruvate hydratase (EC 4.2.1.11) - maize  
N;Alternate names: 2-phospho-D-glycerate hydrolase; enolase  
C;Species: *Mesembryanthemum crystallinum* (common ice plant)  
C;Accession: T12241  
C;Date: 23-Jun-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
R;Porsthoefel, N.R.; Cushman, M.F.; Cushman, April, 1994  
submitted to the EMBL Data Library  
A;Description: Characterization and stress-induced expression of enolase from the facultative  
A;Reference number: T12241  
A;Accession: T12241  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-444 <FOR>  
A;Cross-references: UNIPROT:Q43130; UNIPARC:UPI00016DB3B; EMBL:U09194; NID:9533473; PIR  
C;Function:

A;Title: Differential regulation of enolase during anaerobiosis in maize.  
A;Reference number: Z14628; MUID:99063764; PMID:9847102  
A;Accession: T02221  
A;Status: translated from GB/EMBL/DDJB  
A;Residues: 1-446 <LA>  
A;Cross-references: UNIPROT:P42895; UNIPARC:UPI000129F41; EMBL:U17973; NID:9602252; PIR  
A;Experimental source: strain B73Ht; root  
C;Genetics:  
A;Gene: eno2  
C;Function:  
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glycerate to phosphoenolpyruvate  
A;Note: magnesium cofactor  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; hydro-lyase; magnesium  
F;251,302,329/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted  
F;216,354/Active site: Glu, Lys #status predicted  
Query Match 56.7%; Score 51; DB 2; Length 446;  
Best Local Similarity 68.8%; Pred. No. 2.1; Mismatches 0; Indels 5; Gaps 0;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 395 LAVGLSTGQIKTGAPC 16  
Db 395 LAVGLSTGQIKTGAPC 410

RESULT 27

S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean  
N;Alternate names: enolase  
C;Species: *Ricinus communis* (castor bean)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S39203  
R;Blakely, S.D.; Cole, K.C.; Dennis, D.T.  
submitted to the EMBL Data Library, November 1993  
A;Description: Isolation of a full length cDNA clone encoding cytosolic enolase from Ri.  
A;Reference number: S39203  
A;Accession: S39203  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-445 <BLA>  
A;Cross-references: UNIPROT:P42896; UNIPARC:UPI000129F92; EMBL:228386; NID:9433608; PIR  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.6%; Score 50; DB 2; Length 445;  
Best Local Similarity 68.8%; Pred. No. 3; Mismatches 11; Conservative 0; Indels 5; Gaps 0;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 394 LSVGLATGQIKTGAPC 409

RESULT 28

T12241 phosphopyruvate hydratase (EC 4.2.1.11) - common ice plant  
N;Alternate names: 2-phospho-D-glycerate hydrolase; enolase  
C;Species: *Mesembryanthemum crystallinum* (common ice plant)  
C;Accession: T12241  
C;Date: 23-Jun-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
R;Porsthoefel, N.R.; Cushman, M.F.; Cushman, April, 1994  
submitted to the EMBL Data Library  
A;Description: Characterization and stress-induced expression of enolase from the facultative  
A;Reference number: T12241  
A;Accession: T12241  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-444 <FOR>  
A;Cross-references: UNIPROT:Q43130; UNIPARC:UPI00016DB3B; EMBL:U09194; NID:9533473; PIR  
C;Function:

A;Description: catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 54.4%; Score 49; DB 2; Length 444;  
 Best Local Similarity 68.8%; Pred. No. 43; Mismatches 5; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;

Qy 1 LVVGLCTCQIKTGpac 16  
 Db 393 LSVGLSTGQIKTGpac 408

## RESULT 29

S16257 phosphopyruvate hydratase (EC 4.2.1.11) - maize

N;Alternate names: enolase  
 C;Species: Zea mays (maize)  
 C;Accession: S16257  
 R;Lal, S.K.; Johnson, S.; Conway, T.; Kelley, P.M.

Plant Mol. Biol. 16, 787-795, 1991

A;Title: Characterization of a maize cDNA that complements an enolase-deficient mutant c

A;Reference number: S16257; MUID:9316216; PMID:159865

A;Accession: S16257  
 A;Molecule type: mRNA

A;Residues: 1-446 <LAL>

A;Cross references: UNIPROT:P26301; UNIPARC:UPI000129F3D; EMBL:X55981; NID:92272; PIDN

C;Superfamily: enolase

C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 54.4%; Score 49; DB 2; Length 446;

Best Local Similarity 68.8%; Pred. No. 43; Mismatches 5; Indels 0; Gaps 0;  
 Matches 11; Conservative 0;

Qy 1 LVVGLCTCQIKTGpac 16  
 Db 395 LSVGLSTGQIKTGpac 410

## RESULT 30

S24996 phosphopyruvate hydratase (EC 4.2.1.11) - Chlamydomonas reinhardtii

N;Alternate names: enolase  
 C;Species: Chlamydomonas reinhardtii

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C;Accession: S24996

R;Dumont, F.  
 submitted to the EMBL Data Library, May 1992

A;Reference number: S24989  
 A;Accession: S24996

A;Molecule type: rRNA

A;Residues: 1-372 <DUM>

A;Cross-references: UNIPROT:P31683; UNIPARC:UPI000129F64; EMBL:X56412; NID:918142; PIDN

C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 53.3%; Score 48; DB 2; Length 372;

Best Local Similarity 62.5%; Pred. No. 5.3; Mismatches 5; Indels 0; Gaps 0;  
 Matches 10; Conservative 1; Mismatches 1;

Qy 1 LVVGLCTCQIKTGpac 16  
 Db 323 LAVGLASGQIKTGpac 338

Search completed: April 3, 2006, 08:04:35  
 Job time : 17 secs

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DR	Pfam; PF03952; Endoase_N; 1.	DT	01-OCT-2000 (TREMBrel, 15, Last sequence update)
DR	PRINTS; PR00148; ENOLASE.	DT	01-MAR-2004 (TREMBrel, 26, Last annotation update)
DR	PRODOM; PD000902; Endoase; 1.	DE	Endoase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
DR	TIGRFAMS; TIGR0100-0; end; 1.	DR	(Fragment).
DR	PROSITE; PS00164; ENOLASE; 1.	OS	Homo sapiens (Human).
KW	Direct protein sequencing; Glycolysis: Lyase; Magnesium; Metal-binding; Multigene family; Plasminogen activation.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
KW	METI-MET INIT	OC	NCBI_TaxID=9606;
FT	REGION 404 433	OX	[1]
FT	Required for interaction with PLG (By similarity).	RN	NUCLEOTIDE SEQUENCE.
FT	ACT-SITE 157 157	RP	NUCLEOTIDE SEQUENCE.
FT	By similarity.	RA	Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehrach H., Pouska A., Lundeberg J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
FT	METAL 244 244	RA	Andre N., Bativill X., Escarceller M., Sunoy L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
FT	Magnesium (By similarity).	RL	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
FT	METAL 292 292	RN	[2]
FT	Magnesium (By similarity).	RP	NUCLEOTIDE SEQUENCE.
FT	METAL 317 317	RA	Andre N., Bativill X., Escarceller M., Sunoy L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
FT	Magnesium (By similarity).	CC	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
FT	SEQUENCE 433 AA; 47146 MW; B004E65C46P2E0C CRC64;	CC	-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
Oy	1 LVVGLCTQIKKGAPC 16	CC	-!- PATHWAY: Glycolysis.
Oy	383 LVVGLCTQIKKGAPC 398	CC	-!- SUBUNIT: Homodimer (By similarity).
Db		CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
RESULT 3		CC	-- SIMILARITY: Belongs to the endoase family.
0804Y6 ICTPU		CC	EMBL; AL359113; CAB94588.1; -; mRNA.
ID 0804Y6 ICTPU PRELIMINARY;	PRT; 88 AA..	DR	RESP; P56252; 1P0Z.
AC 0804Y6;		DR	SRR; QNP14; 1-151.
DR 01-JUN-2003 (TREMBrel, 24, Created)		DR	Ensembl; ENSG00000108515; Homo sapiens.
DR 01-JUN-2003 (TREMBrel, 24, Last sequence update)		DR	GO; GO:0000115; C:phosphopyruvate hydratase complex; IEA.
DR 01-MAR-2004 (TREMBrel, 26, Last annotation update)		DR	GO; GO:0016239; F:lyase activity; IEA.
DE Endoase (Fragment).		DR	GO; GO:000087; F:magnesium ion binding; IEA.
OS Ictalurus punctatus (Channel catfish).		DR	GO; GO:000634; F:phosphopyruvate hydratase activity; IEA.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.		DR	GO; GO:006096; P:glycolysis; IEA.
OC Ictalurus.		DR	InterPro; IPR000541; Endoase.
OC Ictalurus.		DR	Pfam; PF00113; Endoase_C; 1.
OK NCBI_TaxID:7998;		DR	PRINTS; PR00148; ENOLASE.
RN [1]		DR	PRODOM; PD000902; Endoase; 1.
RP NUCLEOTIDE SEQUENCE.		DR	PROSITE; PS00164; ENOLASE; 1.
RC TISSUE=Muscle;		KW	Glycolysis; Lyase; Magnesium.
RC "Gene expression in the muscles of young and mature channel catfish (Ictalurus punctatus) as analyzed by expressed sequence tags and gene filter."; R: Fish Physiol. Biochem. 0:0-0 (2003).		FT	NON_TER 1
RT GO; GO:000634; P:phosphopyruvate hydratase activity; IEA.		SO	SEQUENCE 154 AA; 16939 MW; 347B95809B1C864D CRC64;
RT GO; GO:0016829; F:lyase activity; IEA.		Query Match	Best Local Similarity 81.2%; Pred. No. 0 019; Length 154; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RT GO; GO:0006096; P:glycolysis; IEA.		Oy	1 LVVGLCTQIKKGAPC 16
DR InterPro; IPR000941; Endoase.		Db	104 LVVGLCTQIKKGAPC 119
DR Pfam; PF00113; Endoase_C; 1.		RESULT 5	
DR PRODOM; PD000902; Endoase; 1.		OPNG70_9BILA	
FT NON_TER 1		ID OPNG70_9BILA PRELIMINARY;	PRT; 159 AA.
FT SEQUENCE 88 AA; 9830 MW; 8C14B5E5FDE836C1 CRC64;		AC OPNG70_9BILA	
Query Match 72.2%; Score 65; DB 2; Length 88;		DT 01-OCT-2000 (TREMBrel, 15, Created)	
Best Local Similarity 81.2%; Pred. No. 0 011; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		DT 01-OCT-2000 (TREMBrel, 15, Last sequence update)	
Oy 1 LVVGLCTQIKKGAPC 16		DE 01-MAR-2004 (TREMBrel, 26, Last annotation update)	
Oy 383 LVVGLCTQIKKGAPC 53		DE Endoase (Fragment).	
Db		OS Peripatus sp. Par3.	
Db		OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.	
RESULT 4		OK NCBI_TaxID:126380; [1]	
09NP1A_HUMAN		RP NUCLEOTIDE SEQUENCE.	
09NP1A_HUMAN PRELIMINARY;	PRT; 154 AA.	RA Regier J.C., Shultz J.W.;	
09NP1A_HUMAN PRELIMINARY;		RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.	
09NP1A_HUMAN PRELIMINARY;		CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.	
09NP1A_HUMAN PRELIMINARY;		CC -!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).	
09NP1A_HUMAN PRELIMINARY;		CC -!- PATHWAY: Glycolysis.	
01-OCT-2000 (TREMBrel, 15, Created)		DT	

CC	-!- SUBUNIT: Homodimer (By similarity).	CC	H(2)O.
CC	-!- SIMILARITY: Belongs to the enolase family.	CC	-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
CC	EMBL; AR25867; AAF72638.1; -; mRNA.	CC	-!- PATHWAY: Glycolysis.
CC	HSRP; P56252; 1PDZ.	CC	-!- SUBUNIT: Homodimer (By similarity).
CC	SUR; QONG70; 1-159.	CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR	GO; GO:0000115; C:phosphopyruvate hydratase complex; IEA.	CC	-!- SIMILARITY: Belongs to the enolase family.
DR	GO; GO:001829; F:lyase activity; IEA.	DR	EMBL; BC002618; AAH09218.2; -; mRNA.
DR	GO; GO:000287; F:magnesium ion binding; IEA.	DR	HSRP; P56252; 1PDZ.
DR	GO; GO:0004634; P:phosphopyruvate hydratase activity; IEA.	DR	ENSEMBL; ENSG0000074800; Homo sapiens.
DR	GO; GO:0006196; P:glycolysis; IEA.	DR	GO; GO:000287; F:magnesium ion binding; IEA.
DR	InterPro; IPR000941; Enolase.	DR	GO; GO:000287; F:magnesium ion binding; IEA.
DR	pFam; PF00113; Enolase_C; 1.	DR	GO; GO:0000115; C:phosphopyruvate hydratase complex; IEA.
DR	PRINTS; PRO0148; ENOLASE.	DR	GO; GO:000287; F:lyase activity; IEA.
DR	PROSITE; PS00164; ENOLASE; 1.	DR	GO; GO:000287; F:magnesium ion binding; IEA.
KW	Glycolysis; Lyase; Magnesium.	DR	GO; GO:000287; F:glycolysis; IEA.
FT	NON_TER 1	DR	InterPro; IPR000941; Enolase.
FT	NON_TER 1	DR	pFam; PF00113; Enolase_C; 1.
SQ	SEQUENCE 159 AA; 17583 MW; 840E266ACD36D3CD CRC64;	DR	PRINTS; PRO0148; ENOLASE.
Qy	1 LVNGLCTCQIKTGAPC 16	DR	PRODOM; PDD00902; Enolase; 1.
Db	138 LVNGLCTCQIKTGAPC 153	DR	PROSITE; PS00164; ENOLASE; 1.
RESULT 6	Q96GV1 HUMAN	DR	KW GLYCOLYSIS; Lyase; Magnesium.
ID	Q96GV1_HUMAN PRELIMINARY;	DR	FT NON_TER 1
AC	Q96GV1;	Db	SEQUENCE 184 AA; 20415 MW; F94E113824E5290A CRC64;
DT	01-DEC-2001 (TREMBLrel. 19, Created)	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	Db	Best Local Similarity 81.2%; Pred. No. 0.019; 0; Mismatches 0; Indels 0; Gaps 0;
DB	ENOL protein (Fragment).	Qy	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
GN	Name=ENOL;	Db	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Homo Sapiens (Human).	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
OC		Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	Db	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NCBI_TaxID=9606;	[1]	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
OX		Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
RN		Qy	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
RC	NUCLEOTIDE SEQUENCE.	Db	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RC	TISSUE=Ovary;	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
RC	MEDLINE:2238957; PubMed=12479732; DOI=10.1073/pnas.242603899;	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Derkach R.D., Klausner R.D., Collins F.S., Wagner L., Sheppard C.M., Schuler G.D., Al'Fakhil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matsunaga K., Farmer A.A., Roblin G.M., Hong L., Brownstein M.J., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rana S.S., Loqueellano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Borak S.A., McFernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A., Fihley J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Mastra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
RC	NUCLEOTIDE SEQUENCE.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
RC	TISSUE=Brain;	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
RC	Ribas L., Planas J.V., Monetti C., Bernardini G., Saroglia M., Tort L., Mackenzie S.; "A differentially expressed enolase gene isolated from the gilt-head sea bream (sparus aurata) under high-density conditions is up-regulated in brain after in vivo lipopolysaccharide challenge"; Aquaculture 241:195-206 (2004).	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
RC	H(2)O.	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
RC	"-!- PATHWAY: Glycolysis.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
RC	"-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
CC	"-!- SUBUNIT: Homodimer (By similarity).	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
CC	"-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
CC	"-!- SIMILARITY: Belongs to the enolase family.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
DR	EMBL; AX63379; RA092646.1; -; mRNA.	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
DR	HSRP; P56252; 1PDZ.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
DR	SNR; Q7ZMS5; 2-258.	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
DR	GO; GO:0000115; C:phosphopyruvate hydratase complex; IEA.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
DR	GO; GO:0016829; F:lyase activity; IEA.	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
DR	GO; GO:000287; F:magnesium ion binding; IEA.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;
DR	GO; GO:004634; P:phosphopyruvate hydratase activity; IEA.	Qy	Query Match 72.2%; Score 65; DB 2; Length 184;
DR	GO; GO:0006196; P:glycolysis; IEA.	Db	Best Local Similarity 81.2%; Pred. No. 0.022; 0; Mismatches 3; Indels 0; Gaps 0;

DR	InterPro; IPR000941; Enolase.
DR	Pfam; PF00113; Enolase_C; 1.
DR	PRINTS; PR00148; ENOLASE.
DR	PRODOM; PD000902; ENOLAS; 1.
DR	PROSITE; PS00164; ENOLASE; 1.
KW	Glycolysis; Lyase; Magnesium.
FT	NON_TER 1 1
FT	NON_TER 259 259
SQ	259 AA; 28484 MW; 1DE915D3E855331B CRC64;
Ov	Query Match 72.2%; Score 65; DB 2; Length 259; Best Local Similarity 81.2%; Pred. No. 0.03; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	209 LVVGLCTGQIKTGAPC 224
RESULT 8	
ID	Q9BT62_HUMAN PRELIMINARY; PRT; 272 AA.
AC	Q9BT62;
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	ENOL protein (Fragment).
GN	Name=ENOL;
OS	Homo sapiens (Human).
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
OC	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schueler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquelandio N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McElvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]
RN	NUCLEOTIDE SEQUENCE.
RA	Strausberg R., submitted (MAR 2001) to the EMBL/GenBank/DBJ databases.
RL	Submitted (MAR 2001) to the EMBL/GenBank/DBJ databases.
CC	-I- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
CC	-I- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
CC	-I- PATHWAY: Glycolysis.
CC	-I- SUBUNIT: Homodimer (By similarity).
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-I- SIMILARITY: Belongs to the enolase family.
DR	EMBL; BC004325; AAH04325.1; -; mRNA.
DR	HSSP; P5652; 1PDZ.
DR	SMR; Q9BT62; 1-269.
RESULT 9	
ID	Q922A0_MOUSE PRELIMINARY; PRT; 338 AA.
AC	Q922A0;
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Eno2 protein (Fragment).
GN	Name=Eno2;
OS	Mus musculus (Mouse).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Muridae; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
RN	NCBI_TaxID=10090;
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schueler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquelandio N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McElvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [2]
RN	NUCLEOTIDE SEQUENCE.
RC	STRAN=FVB/N; TISSUE=Mammary tumor. C3;
RA	Strausberg R.; Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
RL	Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
CC	-I- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
CC	-I- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
CC	-I- PATHWAY: Glycolysis.
CC	-I- SUBUNIT: Homodimer (By similarity).

CC	-1 - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	DR	EMBL; BC056611; AAH56611.1; - ; mRNA.		
CC	-1 - SIMILARITY: Belongs to the enolase family.	DR	SMR; O6PRC1; 3-363.		
DR	EMBL; BC09018; ANH09018.1; - ; mRNA.	DR	MGI; MGI:95393; Enol.		
DR	HSSP; P56252; 1P0Z.	DR	GO; GO:0005515; F-protein binding; TAS.		
DR	SNR; Q922A0; 25-143; 125-338.	DR	InterPro; IPR00041; Enolase.		
DR	Ensmbl; ENSMUSG00004267; Mus musculus.	DR	Pfam; PF00113; Enolase_C; 1.		
DR	MGI; MGI:95394; Enol2.	DR	Pfam; PF03952; Enolase_N; 1.		
DR	GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.	DR	PRINTS; PR00148; ENOLASE.		
DR	GO; GO:0016829; F:lyase activity; IEA.	DR	PRODOM; PD000902; Enolase; 1.		
DR	GO; GO:00287; F:magnesium ion binding; IEA.	DR	TIGRFAM; TIGR0160; eno; 1.		
DR	PROSTB; PS00164; ENOLASE; 1.	DR	PROSITE; PS00164; ENOLASE; 1.		
RW	Glycolysis; Lyase; Magnesium.	DR	SEQUENCE; 366 AA; 39782 MW; 11E9DDDD4B67D1 CRC64;		
FT	NON_TER 1	Db	SEQUENCE; 338 AA; 37146 MW; B0F2F321D7749484 CRC64;		
Query	Match	Score 65; DB 2; Length 338;	Query	Match	Score 65; DB 2; Length 366;
Best Local Similarity	81.2%;	Pred. No. 0.038;	Best Local Similarity	81.2%;	Pred. No. 0.04;
Matches	13;	Mismatches 0;	Matches	13;	Mismatches 0;
Qy	1 LVNGLCTCQIKTGAPC 16	Db	SEQUENCE; 316 LVNGLCTCQIKTGAPC 331		
Q6PHC1_MOUSE	Q6PHC1_MOUSE PRELIMINARY;	PRT	Q6LDK3_ANAPL PRELIMINARY;	PRT	Q6LDK3_ANAPL PRELIMINARY;
AC	Q6PHC1;	PRT; 366 AA.	AC	Q6LDK3;	PRT; 377 AA.
DT	05-JUL-2004 (TREMBrel. 27; Last sequence update)	DT	05-JUL-2004 (TREMBrel. 27; Last sequence update)	DT	05-JUL-2004 (TREMBrel. 27; Last sequence update)
DT	05-JUL-2004 (TREMBrel. 27; Last sequence update)	DT	05-JUL-2004 (TREMBrel. 27; Last sequence update)	DT	05-JUL-2004 (TREMBrel. 27; Last sequence update)
DT	05-JUL-2004 (TREMBrel. 27; Last annotation update)	DT	05-JUL-2004 (TREMBrel. 27; Last annotation update)	DT	05-JUL-2004 (TREMBrel. 27; Last annotation update)
DE	Enol protein.	DE	Alpha-enolase/tau-crystallin (BC 4.2.2.1.11).	DE	Alpha-enolase/tau-crystallin (BC 4.2.2.1.11).
GN	Name=Enol;	OS	Anas platyrhynchos (Domestic duck).	OS	Anas platyrhynchos (Domestic duck).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glutes; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC
OC		OX	Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.	OX	Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OC		NCBI_TAXID=8839;	NCBI_TAXID=8839;	NCBI_TAXID=8839;	NCBI_TAXID=8839;
OC		[1]	[1]	[1]	[1]
NCBI_TAXID=10090;	OX	RN	NUCLEOTIDE SEQUENCE	RN	NUCLEOTIDE SEQUENCE
OX		RP	MEDLINE=89019778; PubMed=2463567; DOI=10.1083/jcb.107.6.2729; Wistow G.J., Lietman T., Williams L.A., Stapel S.O., de Jong W.W., Horwitz J., Platigorsky J.	RP	MEDLINE=89019778; PubMed=2463567; DOI=10.1083/jcb.107.6.2729; Wistow G.J., Lietman T., Williams L.A., Stapel S.O., de Jong W.W., Horwitz J., Platigorsky J.
RN		RR	"Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens structural protein."	RR	"Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens structural protein."
RN		RL	J. Cell Biol. 107:2729-2736(1998).	RL	J. Cell Biol. 107:2729-2736(1998).
RN		[12]	[12]	[12]	[12]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=FVB/N; TISSUE=Matmary tumor. C3;	RA	MEDLINE=91365245; PubMed=1889745; DOI=10.1016/0378-1119(91)90273-E; Kim R.Y., Leitman T., Platigorsky J., Wistow G.J.; "Structure and expression of the duck alpha-enolase/-tau-crystallin-encoding gene," Gene 103:193-200 (1991).	RA	MEDLINE=91365245; PubMed=1889745; DOI=10.1016/0378-1119(91)90273-E; Kim R.Y., Leitman T., Platigorsky J., Wistow G.J.; "Structure and expression of the duck alpha-enolase/-tau-crystallin-encoding gene," Gene 103:193-200 (1991).
RX	STRAIN=FVB/N; TISSUE=Matmary tumor. C3;	RA	EMBL; M55143; AAA42217.1; - ; Genomic DNA.	RA	EMBL; M55143; AAA42217.1; - ; Genomic DNA.
RA	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;	RA	EMBL; M55134; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55134; AAA9217.1; JOINED; Genomic DNA.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Tsohbyki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarante P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Farhey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchnik J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska G.O., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA	EMBL; M55135; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55135; AAA9217.1; JOINED; Genomic DNA.
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RT		RA	EMBL; M55204; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55204; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55205; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55205; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55206; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55206; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55207; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55207; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55208; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55208; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55209; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55209; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55210; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55210; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55211; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55211; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55212; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55212; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55213; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55213; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55214; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55214; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55215; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55215; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55216; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55216; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55217; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55217; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55218; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55218; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M55219; AAA9217.1; JOINED; Genomic DNA.	RA	EMBL; M55219; AAA9217.1; JOINED; Genomic DNA.
RT		RA	EMBL; M		

							Query Match Best Local Similarity 81.2%; Score 65; DB 2; Length 377; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Score 72.2%; Score 65; DB 2; Length 377; OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OY	1	1	LWVGLCTCQIKTGAPC 16					OC NCBI_TAXID=7753; [1]
		Db	327	LWVGLCTCQIKTGAPC 342				OC NUCLEOTIDE SEQUENCE. RX MEDLINE=20063780; PubMed=10594174; RA Kuraku S., Hosoya D., Katoh K., Suga H., Miyata T.; RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes"; J. Mol. Evol. 49:729-735(1999).
								CC H(2)O.
								CC -I- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
								CC -I- PATHWAY: Glycolysis.
								CC -I- SUBUNIT: Homodimer (By similarity).
								CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
								CC -I- SIMILARITY: Belongs to the enolase family.
								DR EMBL; AB025329; BAA88482.1; -; mRNA.
								DR HSSP; P56252; LPDZ.
								DR SMR; O9PTX5_1-39.
								DR GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.
								DR GO; GO:000287; F:lyase activity; IEA.
								DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
								DR GO; GO:0006096; P:glycolysis; IEA.
								DR InterPro; IPR00911; enolase.
								DR Pfam; PF00113; Enolase_C; 1.
								DR Pfam; PF003952; Enolase_N; 1.
								DR PRINTS; PR0148; ENOLASE.
								DR PRODOM; PD00090; Enolase; 1.
								DR TIGRFAMS; TIGR01060; eno; 1.
								DR PROSITE; PS00164; ENOLASE; 1.
								KW Glycolysis; Lyase; Magnesium.
								FT NON_TER 1 1 1
		SQ	SEQUENCE	394 AA; 42583 MW; BC585FEG6C712A3D2 CRC64;				
								Query Match Best Local Similarity 81.2%; Score 65; DB 2; Length 394; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	1	1	LWVGLCTCQIKTGAPC 16					OC NUCLEOTIDE SEQUENCE. RX MEDLINE=94195794; PubMed=8146164;
		Db	345	LWVGLCTCQIKTGAPC 360				RA Hedges S.B.; RT "Molecular evidence for the origin of birds"; Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
								CC H(2)O.
								CC -I- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
								CC -I- PATHWAY: Glycolysis.
								CC -I- SUBUNIT: Homodimer (By similarity).
								CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
								-I- SIMILARITY: Belongs to the enolase family.
								OS Lampetra reissneri (Par Eastern brook lamprey).

CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DR	EMBL; L28078; ARX35671.1; -; mRNA.
DR	PIR; I50026; I50026.
DR	HSSP; P56252; 1PDZ.
DR	SNR; P42897; 1-395.
DR	InterPro; IPR000941; Enolase.
DR	PANTHER; PTM11902; Enolase; 1.
DR	Pfam; PF00113; Enolase_C; 1.
DR	Pfam; PF03952; Enolase_N; 1.
DR	PRINTS; PRO0148; ENOLASE.
DR	PRODOM; PD000902; Enolase; 1.
DR	TIGRFAMS; TIGR01060; eno; 1.
DR	PROSITE; PS00164; ENOLASE; 1.
DR	KW GLYCOLYSIS; Lyase; Magnesium.
FT	NON_TER 1
SQ	SEQUENCE 395 AA; 43131 MW; D351C6700BDC75CD CRC64;
Query Match	72.2%; Score 65; DB 2; Length 395;
Best Local Similarity	81.2%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;
Matches	13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 LVVGLCTCQIKTGpac 16
Db	345 LVVGLCTCQIKTGpac 360
RESULT 15	RESULT 16
O9U5F7_EPTBU PRELIMINARY;	O9PTX5_LAMRE
ID O9U5F7;	ID O9PTX5_LAMRE PRELIMINARY;
AC 09U5F7;	PRT; 395 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OX NCBI_TaxID=7753;	DE Enolase-2 (Fragment)
RN [1]	GN Name=enolase-2;
RP NUCLEOTIDE SEQUENCE.	OS Lampetra reissneri (Far Eastern brook lamprey).
RK MEDLINE=20063780; PubMed=10594174;	OC Petromyzontiformes; Petromyzontidae; Lethenteron.
RA Kuroku S., Hoshiiyama D., Katoh K., Suga H., Miyata T.;	OC Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded	OC Myxiniidae; Eptatretinae; Eptatretus.
RT genes"; Evol. 49:729-735(1999).	OX NCBI_TaxID=7754;
RL J. Mol. Evol. 49:729-735(1999).	RN [1]
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +	RP NUCLEOTIDE SEQUENCE.
CC H(2)O.	RK MEDLINE=20063780; PubMed=10594174;
CC -!- COFACTOR: Magnesium. Required for catalysis and for stabilizing	RA Kuroku S., Hoshiiyama D., Katoh K., Suga H., Miyata T.;
CC the dimer (By similarity).	RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
CC -!- PATHWAY: Glycolysis.	RT genes"; Evol. 49:729-735(1999).
CC -!- SUBUNIT: Hemodimer (By similarity).	RL J. Mol. Evol. 49:729-735(1999).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	DR GO:0006096; P:glycolysis; IEA.
CC -!- SIMILARITY: Belongs to the enolase family.	DR HSSP; P56252; 1PDZ.
DR GO:0006096; P:glycolysis; IEA.	DR SNR; O9PTX5; 1-394.
RL J. Mol. Evol. 49:729-735(1999).	DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +	DR GO: GO:0016829; F:lyase activity; IEA.
CC H(2)O.	DR GO: GO:000287; F:magnesium ion binding; IEA.
-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing	DR GO: GO:0006096; P:phosphopyruvate hydratase activity; IEA.
the dimer (By similarity).	DR GO: GO:0006096; P:glycolysis; IEA.
-!- PATHWAY: Glycolysis.	DR InterPro; IPR000941; Enolase.
CC -!- SUBUNIT: Homodimer (By similarity).	DR Pfam; PF00113; Enolase_C; 1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	DR Pfam; PF03952; Enolase_N; 1.
-!- SIMILARITY: Belongs to the enolase family.	DR PRINTS; PRO0148; ENOLASE.
EMBL; AB025330; BAA8483.1; -; mRNA.	DR PROSITE; PS00164; ENOLASE.
DR HSSP; P56252; 1PDZ.	DR TIGRFAMS; TIGR01060; eno; 1.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.	DR PROSITE; PS00164; ENOLASE; 1.
DR GO; GO:0016829; F:lyase activity; IEA.	DR KW GLYCOLYSIS; Lyase; Magnesium.
DR GO; GO:0000287; F:magnesium ion binding; IEA.	FT NON_TER 1
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.	SQ SEQUENCE 395 AA; 43267 MW; 8591D68662DAB544 CRC64;
DR GO; GO:0006096; P:glycolysis; IEA.	Query Match 72.2%; Score 65; DB 2; Length 395;
DR Best Local Similarity 81.2%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVVGLCTCQIKTGpac 16	

Db 345 LVVGLCTGQIKTGAPC 360

RT	sapiens;"
RL	Cell 119:1027-1040(2004)
CC	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
CC	-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
CC	-!- PATHWAY: Glycolysis.
DT	13-SEP-2005 (TREMBrel_31, Created)
DT	13-SEP-2005 (TREMBrel_31, Last sequence update)
DE	Chromosome undetermined SCRF1462, whole genome shotgun sequence.
GN	ORFNames=GSTENG000964001
OS	Tetraodon nigroviridis (Green puffer).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
OC	NCBI_TaxID=99883;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Jailon O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Basilia S., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Bleumont C., Skalli Z., Cattolico L., Poulain J., De Bernardini V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Voilff J.N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lauder V., Schachter V., Quétier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; Nature 431:946-957 (2004).
RN	[2]
RG	Nucleotide sequence.
RLL	Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
DR	EMBL: CAE01011462; CAF93020_1; -; Genomic DNA.
SQ	SEQUENCE 406 AA; 43712 MW; 18C266C4F923E27D CRC64;
Query Match	72.2%; Score 65; DB 2; Length 406; Best Local Similarity 81.2%; Pred. No. 0.044; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LVVGLCTGQIKTGAPC 16
Db	358 LVVGLCTGQIKTGAPC 373
RESULT 18	
OSISQ MACFA	
ID OSISQ MACFA PRELIMINARY; PRT; 420 AA.	
AC OSISQ;	
DT 10-MAY-2005 (TREMBrel_30, Created)	
DT 10-MAY-2005 (TREMBrel_30, Last sequence update)	
DT 10-MAY-2005 (TREMBrel_30, Last annotation update)	
DE Enolase 2 (Fragment). 30, Last annotation update)	
OS Macaca fascicularis (Crab eating macaque) ( <i>Cynomolgus monkey</i> )	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Buteraria; Buaerchontoglires; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Macaca.	
OC NCBI_TaxID=9541;	
RN [1]	NUCLEOTIDE SEQUENCE.
RN NUCLEOTIDE SEQUENCE.	
PubMed-15120360; DOI-10.1016/j.cell.2004.11.040;	
RA Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L., Mahowald M., Wyckoff G.J., Malcolm C.M., Lahn B.T.; "Accelerated evolution of nervous system genes in the origin of Homo	
RT	Nature 431:946-957(2004).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RT	sapiens;"
RL	Cell 119:1027-1040(2004)
CC	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
CC	-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).
CC	-!- PATHWAY: Glycolysis.
DT	13-SEP-2005 (TREMBrel_31, Created)
DT	13-SEP-2005 (TREMBrel_31, Last sequence update)
DE	Chromosome undetermined SCRF7145, whole genome shotgun sequence.
GN	ORFNames=GSTENG00089001
OS	Tetraodon nigroviridis (Green Puffer).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
OC	NCBI_TaxID=99883;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Jailon O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Basilia S., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Bleumont C., Skalli Z., Cattolico L., Poulain J., De Bernardini V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Voilff J.N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lauder V., Schachter V., Quétier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.

RG NUCLEOTIDE SEQUENCE.  
 RL TISSUE=Embryo;  
 CC Director MGC Project;  
 CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC EMBL; BC071359; AAH71359.1; -; mRNA.  
 CC SMC; Q61QPS; 2-431.  
 CC ZFIN; ZDB-GENE-030131-6048; zgc:73152.  
 CC GO; GO-000015; C:phosphopyruvate hydratase complex; IEA.  
 CC GO; GO-0004334; F:phosphopyruvate hydratase activity; IEA.  
 CC InterPro; IPR00941; Enolase.  
 CC Pfam; PF00148; ENOLASE.  
 CC DR Pfam; PF03952; Enolase\_N; 1.  
 CC DR PRINTS; PRO0148; ENOLASE.  
 CC DR PRODOM; PD000902; Enolase; 1.  
 CC DR TIGRFAMS; TIGR01060; eno; 1.  
 CC DR PROSITE; PS00164; ENOLASE; 1.  
 CC KW Glycolysis; Lyase; Magnesium.  
 CC FT NON\_TER 431  
 CC SQ SEQUENCE 431 AA; 4711 MW; F7A79F670744BBC1 CRC64;  
 CC Query Match 72.2%; Score 65; DB 2; Length 431;  
 CC Best Local Similarity 81.2%; Pred. No. 0.047;  
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 20  
 Q61QPS\_BRARE  
 ID Q61QPS\_BRARE PRELIMINARY; PRT; 432 AA.  
 AC 061QPS\_061QPS\_2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Enolase 1, (Alpha);  
 GN ORFName=zgc:73152;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Wild-type; TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Maruyama K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaraine P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marras M.A.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marras M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RA and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

RESULT 21  
 Q6PC12\_BRARE  
 ID Q6PC12\_BRARE PRELIMINARY; PRT; 432 AA.  
 AC 06PC12\_06PC12\_2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DE Enolase 1, (Alpha);  
 GN ORFName=zgc:73152;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Wild-type; TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Maruyama K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaraine P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marras M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RA and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

NUCLEOTIDE SEQUENCE.  
 TISSUE=Embryo;  
 Director MGC Project;  
 Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 EMBL; BC059511; AAC159511.1; -; mRNA.  
 SMR; Q6PC12; 2-431.





- RA Villalon D.K., Murry D.M., Sodegren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bonnard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalaka U., Smilus D.E., Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).
- [6] NUCLEOTIDE SEQUENCE OF 165-433; MEDLINE=98317532; PubMed=9553645; DOI=10.1006/geno.1997.5186; Onyango P., Lubysova B., Gardellin P., Kurzbauer R., Weith A.; "Molecular cloning and expression analysis of five novel genes in chromosome 1p36."; *Genomics* 50:187-198 (1998).
- RN [9]
- RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 170-433.
- RC TISSUE-BRAIN; MEDLINE=97264341; PubMed=9110174;
- RA Yu W., Anderson B., Worley K.C., Muzyz D.M., Ding Y., Liu W., Riccafrete J.Y., Wentland M.A., Lennon G., Gibbs R.A.; "Large-scale concatenation cDNA sequencing"; *Genome Res.* 7:353-358 (1997).
- RN [10]
- RP PROTEIN SEQUENCE OF 269-280 AND 306-320, AND INDUCTION IN DIFFUSE LARGE CELL LYMPHOMA; MEDLINE=95307697; PubMed=7787969;
- RA Mohamad R.M., Handan M.Y., Maki A., Al-Katib A.; "Induced expression of alpha-enolase in differentiated diffuse large cell lymphoma."; *J. Cell. Mol. Life Sci.* 58:902-920 (2001).
- RL Enzyme Protein 48:37-44 (1995).
- RN [11]
- RP PROTEIN SEQUENCE OF 1-8 (ISOFORM ALPHA-ENOLASE).
- RC TISSUE-Colon carcinoma; MEDLINE=97295306; PubMed=9150948; JI H., Reid G.E., Moritz R.L., Bodes J.S., Burgess A.W., Simpson R.J.; "A two-dimensional gel database of human colon carcinoma proteins"; *Electrophoresis* 18:605-613 (1997).
- RN [12]
- RP FUNCTION OF MBP1, IDENTIFICATION OF REPRESSOR DOMAINS, AND MUTAGENESIS OF LEB-3B AND LBU-3B; MEDLINE=99182475; PubMed=10082554; Ghosh A.K., Steele R., Ray R.B.; "Functional domains of c-myc promoter binding protein 1 involved in transcriptional repression and cell growth regulation."; *Mol. Cell. Biol.* 19:2880-2886 (1999).
- RN [13]
- RP FUNCTION AS A C-MYC TRANSCRIPTIONAL REPRESSOR, AND SUBCELLULAR LOCATION; MEDLINE=20263725; PubMed=10802057; DOI=10.1016/S0014-5793(00)01494-0; Feo S., Arcuri D., Paddini E., Passantino R., Giallongo A.; "ENOL gene product binds to the c-myc promoter and acts as a transcriptional repressor: relationship with Myc promoter-binding protein 1 (MBP-1)."; *FEMS Lett.* 473:47-52 (2000).
- RN [14]
- RP FUNCTION IN PLASMINOGEN ACTIVATION; MEDLINE=22251878; PubMed=12666133; DOI=10.1002/ajh.10299; Lopez-Altemany R., Longstaff C., Hawley S., Mirshahi M., Fabregas P., Jardi M., Merton B., Miles L.A., Felez J.; "Identification of an epope of alpha-enolase (a candidate plasminogen receptor) by phage display."; *Am. J. Hematol.* 72:234-242 (2003).
- RN [15]
- RP INTERACTION WITH PLG; MEDLINE=97452346; PubMed=9308760; Arza B., Felez J., Lopez-Altemany R., Miles L.A., Munoz-Canovas P.; "Inhibition of cell surface mediated plasminogen activation by a monoclonal antibody against alpha-enolase."; *Thromb. Haemost.* 78:1097-1103 (1997).
- RN [16]
- RP EPITOPE MAPPING, AND ASSOCIATION WITH CAR; MEDLINE=99036529; PubMed=9878089; DOI=10.1006/jaut.1998.0239; RA Adams G., Amundson D., Seigel G.M., Machnicki M.; "Anti-enolase-alpha autoantibodies in cancer-associated retinopathy: epitope mapping and cytotoxicity on retinal cells."; *J. Autoimmun.* 11:671-677 (1998).
- RN [17]
- RP IDENTIFICATION OF MBP1 AS AN ALPHA ENOLASE ALTERNATIVE INITIATION PRODUCT, AND MUTAGENESIS OF MET-93 AND MET-95; MEDLINE=20148810; PubMed=10681589; DOI=10.1074/jbc.275.8.5958; Subramanian A., Miller D.M.; "Structural analysis of alpha-enolase, Mapping the functional domains involved in down-regulation of the c-myc protooncogene."; *J. Biol. Chem.* 275:5958-5965 (2000).
- RN [18]
- RP REVIEW; MEDLINE=21398199; PubMed=11497239; RA Pancholi V.; "Multifunctional alpha-enolase: its role in diseases."; *Cell. Mol. Life Sci.* 58:902-920 (2001).
- RN [19]
- RP INTERACTION OF MBP1 WITH SBDL; MEDLINE=20576811; PubMed=1113451; DOI=10.1128/MCB.21.2.655-662.2001; RA Ghosh A.K., Majumder M., Steele R., White R.A., Ray R.B.; "A novel 16-kilodalton cellular protein physically interacts with and antagonizes the functional activity of c-myc promoter-binding protein 1."; *Cell. Biol.* 21:655-662 (2001).
- RN [20]
- RP IDENTIFICATION AS AN AUTOANTIGEN IN HASHIMOTO ENCEPHALOPATHY; MEDLINE=22233760; PubMed=12297304; DOI=10.1016/S0014-5793(02)03307-0; RX RA Ochi H., Horiechi I., Araki N., Toda T., Araki T., Sato K., Murai H., Osoegawa M., Yamada T., Okamura K., Ogino T., Mizumoto K., RA Yamashita H., Saya H., Kira J.; "Proteomic analysis of human brain identifies alpha-enolase as a novel autoantigen in Hashimoto's encephalopathy."; *FEBS Lett.* 528:197-202 (2002).
- RN [-] FUNCTION: Multifunctional enzyme that, as well as its role in glycolysis, plays a part in various processes such as growth control, hypoxia tolerance and allergic responses. May also function in the intravascular and pericellular fibrinolytic system due to its ability to serve as a receptor and activator of plasminogen on the cell surface of several cell-types such as leukocytes and neurons.
- CC [-] FUNCTION: MBP1 binds to the c-myc promoter and acts as a transcriptional repressor. May be a tumor suppressor.
- CC [-] CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H<sub>2</sub>O.
- CC [-] COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer.
- CC [-] PATHWAY: Glycolysis.
- CC [-] SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits, alpha, beta and gamma, which can form homodimers or heterodimers which are cell-type and development-specific. ENOL interacts with PLG in the neuronal plasma membrane and promotes its activation. The C-terminal lysine is required for this binding (By similarity).
- CC [-] SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma membrane in either the homodimeric (alpha/alpha) or heterodimeric membrane.
- CC Query Match Best Local Similarity Score DB Length ID Matches保守性 81.2%; Score 65; DB 1; Length 433;保守性 0; Mismatches 3; Indels 0; Gaps 0;
- OY 1 LVVGLCTCQIKTGPC 16
- Dy 383 LVVGLCTCQIKTGPC 398
- RESULT 26
- ID ENOA\_MOUSE STANDARD; PRT; 433 AA.
- AC P17182; Q99KT7; Q9DCV7;

- DT 01-AUG-1990 (Rel. 15, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 13-SEP-2005 (REL 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-  
 DE neural enolase) (NNE) (Enolase 1).  
 GN Name=Enol; Synonyms=Eno-1,  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=900501487; PubMed=2362815;  
 RA Kaghad M., Dumont X., Chalon P., Lelias J.M., Lamande N., Lucas M., Lazar M., Caput D.;  
 RL "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from  
 RT mouse brain";  
 RP Nucleic Acids Res. 18:3638-3638(1990).  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kubokawa T., Adachi J., Bono H., Kondo S., Nakanishi I., Osato N., Saito R., Suzuki H., Yamamoto K., Kyosuwa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldwin R.L., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanagin H., Battalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbett L.E., Cousins S., Dalla E., Drabani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Hedges S., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konigaya A., Kurockin I.V., Lee Y., Lehardt B., Lyons P.A., Magliott D.R., Maltis J., Macchioni L., McKenize L., Miki H., Nagashima T., Numata K., Okido T., Pavon W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Winslow-Boris A., Yanagisawa M., Yang T., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kondo H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Itoh M., Kogawa I., Mizazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunisi A., Yobino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
 RT Nature 420:563-573 (2002).  
 RL [3]  
 RN NUCLEOTIDE SEQUENCE. [LARGE SCALE mRNA].  
 RC STRAIN=Czech II, and FVB/N; TISSUE=Mammary gland, and Mammary tumor;  
 RX MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altshul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan D., Moore S.T., Wang J., Hsieh F., Diatchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshihiko S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Max J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,
- RN Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RC "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16189-16903 (2002).  
 RN [4]  
 RP PROTEIN SEQUENCE OF 59-70; 99-113; 183-197 AND 245-258.  
 RC TISSUE=Macrophage;  
 RX PubMed=6427801;  
 RA Bottalico L.A., Kendrick N.C., Keller A., Li Y., Tabas I.; Lazar M., Keller A.;  
 RL "Cholesteryl ester loading of mouse peritoneal macrophages is associated with changes in the expression or modification of specific cellular proteins, including increase in an alpha-enolase isoform";  
 RT Arterioscler. Thromb. 13:264-275 (1993).  
 RP INTERACTIONS WITH PKM2; PKM; CTD; ALDO AND TROPONIN, AND DEVELOPMENTAL STAGE;  
 RX MEDLINE=97270626; PubMed=9169614;  
 RA Merkulova T., Lucas M., Jabet C., Lamande N., Roureau J.-D., Gros F., Lazar M., Keller A.;  
 RL "Biochemical characterization of the mouse muscle-specific enolase: developmental changes in electrophoretic variants and selective binding to other proteins";  
 BIochim. J. 323:791-800 (1997).  
 RN [6]  
 RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY  
 RX MEDLINE=21121273; PubMed=11226603; DOI=10.1016/S0248-4900(00)01103-5;  
 RA Keller A., Demerie R., Merkulova T., Geraud G., Cywinski-Golenzter C., Lucas M., Chatelet F.-P.;  
 CC "Fibre-type distribution and subcellular localisation of alpha and beta enolase in mouse striated muscle";  
 CC Biol. Cell 92:27-35 (2000).  
 CC -!- FUNCTION: Multi-functional enzyme that, as well as its role in glycolysis, plays a part in various processes such as growth control, hypoxia tolerance and allergic responses (By similarity). May also function in the intravascular and pericellular fibrinolytic system due to its ability to serve as a receptor and activator of plasminogen on the cell surface of several cell-types such as leukocytes and neurons (By similarity).  
 CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H<sub>2</sub>O.  
 CC -!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer.  
 CC -!- PATHWAY: Glycolysis.  
 CC -!- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits, alpha, beta and gamma, which can form homodimers or heterodimers which are cell-type and development-specific. ENO1 interacts with PIG in the neuronal plasma membrane and promotes its activation. The C-terminal lysine is required for this binding (By similarity). In vitro, interacts with several glycolytic enzymes including PKM2, PGM, CKM and aldolase. Also binds troponin, in vitro.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma membrane in either the homodimeric (alpha/alpha) or heterodimeric (alpha/gamma) form (By similarity). ENO1 is localized to the M-band.  
 CC -!- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in embryo and in most adult tissues. The alpha/beta heterodimer and the beta/beta homodimer are found in striated muscle, and the alpha/gamma heterodimer and the gamma/gamma homodimer in neurons. In striated muscle, expression of ENO1 appears to be independent of fiber type.  
 CC -!- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition from the alpha/alpha homodimer to the alpha/beta heterodimer in striated muscle cells, and to the alpha/gamma heterodimer in nerve cells. In embryonic muscle, ENO1 is highly expressed until E17. Decreased levels from P5.  
 CC -!- SIMILARITY: Belongs to the enolase family.  
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[5] PROTEIN SEQUENCE OF 45-56; 96-108; 244-261 AND 368-381, AND  
RP PROTEIN INTERACTION WITH PLG.  
RC TISSUE-Embryonic brain;  
RX MEDLINE=95054017; PubMed=7964722;  
RA Nakajima K.; Hamanoue M., Takemoto N., Hattori T., Kato K.,  
RA Kohsaka S.; "Plasminogen binds specifically to alpha-enolase on rat neuronal  
RT plasma membrane";  
RL J. Neurochem. 63:2048-2057(1994).  
RN [6] DEVELOPMENTAL STAGE.  
RX MEDLINE=96134716; PubMed=8594891;  
RA Keller A., Rouzeau J.D., Farhadian F., Wisnewsky C., Marotte F.,  
RA Lamande N., Samuel J.L., Schwartzen K., Lazar M., Lucas M.;  
RT "Differential expression of alpha- and beta-enolase genes during rat  
heart development and hypertrophy";  
RL Am. J. Physiol. 269:H1841-H1851(1995).  
RN [7] EFFECT OF THYROID HORMONES ON EXPRESSION.  
RX MEDLINE=20131238; PubMed=10662718;  
RA Merklova T., Keller A., Oliviero P., Marotte F., Samuel J.L.,  
RA Rappoport L., Lamande N., Lucas M.;  
RT "Thyroid hormones differentially modulate enolase isozymes during rat  
skeletal and cardiac muscle development.;"  
RL Am. J. Physiol. 278:B330-B339(2000).  
RN [8] SUBCELLULAR LOCATION OF ALPHA/GAMMA HETERO-DIMER.  
RX PubMed=15041191; DOI=10.1016/j.neuro.2003.12.006;  
RA Ueta H., Nagasawa H., Oyabu-Manabe Y., Toida K., Ishimura K., Hori H.;  
RT "Localization of enolase in synaptic plasma membrane as an alphagamma  
heterodimer in rat brain.;"  
RL Neurosci. Res. 48:379-386(2004).  
CC -!- FUNCTION: Multifunctional enzyme that, as well as its role in  
glycolysis, plays a part in various processes such as growth  
control, hypoxia tolerance and allergic responses. May also  
function in the intravascular and pericellular fibrinolytic system  
due to its ability to serve as a receptor and activator of  
plasminogen on the cell surface of several cell-types such as  
leukocytes and neurons.  
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
H(2)O.  
CC -!- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
the dimer.  
CC -!- PATHWAY: Glycolysis.

-!- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
alpha, beta and gamma, which can form homodimers or heterodimers  
which are cell-type and development-specific. ENOL interacts with  
PLG in the neuronal plasma membrane and promotes its activation.  
The C-terminal lysine is required for this binding (By  
similarity).

-!- SUBCELLULAR LOCATION: Cyttoplasmic. Can translocate to the plasma  
membrane in either the homodimeric (alpha/alpha) or heterodimeric  
(alpha/gamma) form.

-!- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in  
embryo and in most adult tissues. The alpha/beta heterodimer and  
the beta/beta homodimer are found in striated muscle, and the  
alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.

-!- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition  
from the alpha/alpha homodimer to the alpha/beta heterodimer in  
striated muscle cells, and to the alpha/gamma heterodimer in nerve  
cells. In brain, levels of ENOL decrease around 10 dpc and then  
gradually increase to adult age. In embryonic heart, ENOL levels  
decrease rapidly during cardiac development.

-!- SIMILARITY: Belongs to the enolase family.

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between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.

DR EMBL; BC063174; AAH63174.1; ALT INIT; mRNA.  
DR EMBL; BC078826; AAH78896.1; -; mRNA.  
DR EMBL; BC081847; AAH81847.1; ALT INIT; mRNA.  
DR EMBL; AR24613; ARK01319.1; -; mRNA.  
DR PIR; A22126; A2326.  
DR HSSP; PS6252; 1PDZ.  
DR SMR; P04764; 1-A30.  
DR Ensembl; ENSRNOG0000017895; Rattus norvegicus.  
DR RGD; 2553; Enol.  
DR InterPro; IPR00041; Enolase.  
DR PANTHER; PTHR11902; Enolase; 1.  
DR Pfam; PF00113; Enolase C; 1.  
DR Pfam; PP03932; Enolase N; 1.  
DR PRINTS; PRO014; ENOLASE.  
DR PRODOM; PD000902; Enolase; 1.  
DR TIGRFAM; TIGR01060; enol; 1.  
DR PROSITE; PS01614; ENOLASE; 1.  
KW Direct protein sequencing; Glycolysis; lyase; Magnesium  
binding; Multigene family; Plasminogen activation.  
FT By similarity.  
FT Required for interaction with PLG.  
FT REGION 404 433 By similarity.  
FT ACT SITE 157 157 By similarity.  
FT METAL 244 244 By similarity.  
FT METAL 292 292 By similarity.  
FT METAL 317 317 By similarity.  
FT METAL 47 47 By similarity.  
FT CONFLICT 92 95 By similarity.  
FT CONFLICT 124 124 By similarity.  
FT CONFLICT 143 143 By similarity.  
FT CONFLICT 150 150 By similarity.  
FT CONFLICT 249 249 By similarity.  
FT CONFLICT 373 373 By similarity.  
FT CONFLICT 373 373 G > E (in Ref. 1).  
SQ SEQUENCE 433 AA; 46997 MW; 6198009DACDDBBC CRC64;  
Query Match 72.2%; Score 65; DB 1; length 433;  
Matches 13; Conservative 81.2%; Pred. No. 0.047; 0; Mismatches 3; Indels 0; Gaps 0;  
QV 1 LVVGLCTQIKTGAC 16  
Db 383 LVVGLCTQIKTGAC 398

RESULT 29

ID	ENOA_SCEN	STANDARD;	PRT;	433 AA.
AC	Q9W712; 28-FEB-2003 (Rel. 41, last sequence update)			
DT	13-SEP-2005 (Rel. 48, last annotation update)			
DE	Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Phosphopyruvate hydratase).			
OS	Sceloporus undulatus (Eastern fence lizard) (Skink); Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OOC Lepidosaurs; Squamata; Iguania; Iguanidae; Phrynosomatidae; Sceloporus; NCBI-TaxID=8520;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Muscle;			
RX	MEDLINE=99439677; PubMed=10508547; DOI=10.1006/mpev.1999.0640;			
RA	Mammen H., Li S.-S.-L.; "Molecular evidence for a clade of turtles.>"; RT Mol. Phylogenet. Evol. 13:44-48(1999).			
RL	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.			
CC	-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).			
CC	-!- PATHWAY: Glycolysis.			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- SIMILARITY: Belongs to the enolase family.			

EMBL; X02610; CNA26456.1; -; mRNA.

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CC EMBL; AF072587; ADD41644.1; -; mRNA.  
DR HSSP; P56252; 1P0Z.  
DR SMR; Q9W7L2; 1-A32.  
DR InterPro; IPR00941; Enolase.  
DR PANTHER; PTHR11902; Enolase.  
DR Pfam; PF00113; Enolase\_C; 1.  
DR PRINTS; PRO0148; ENOLASE.  
DR TIGRFAMS; TIGR01060; eno; 1.  
DR PROSITE; PS00164; ENOLASE; 1.  
DR KW GLYCOLYSIS; Lyase; Magnesium; Metal-binding; Multigene family.  
INIT MET 0 By similarity.  
FT METAL 244 Magnesium (By similarity).  
FT METAL 292 Magnesium (By similarity).  
FT METAL 317 Magnesium (By similarity).  
SQ SEQUENCE 433 AA; 47362 MW; 7CD89EB405529301 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.047;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCITCQIKTGAPC 16  
Db 383 LVVGLCITCQIKTGAPC 398

RESULT 30

ID	ENOA_TRASC	STANDARD:	PRT:	433 AA.
AC	Q9W7L1;			
DT	28-FEB-2003	(Rel. 41, Created)		
DT	13-SEP-2005	(Rel. 48, Last annotation update)		
DE	Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (phosphopyruvate hydratase)			
OS	Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta); Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.			
OC	NCBI_TaxID:34903;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	STRAIN=Subsp. elegans; TISSUE=muscle; MEDLINE=99039677; PubMed=10508547; DOI=10.1006/mpev.1999.0640;			
RA	Mannen H., Li S.S.-L.;			
RT	"Molecular evidence for a clade of turtles."; Mol. Phylogenet. Evol. 13:144-148 (1999).			
RL				
CC	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.			
CC	-!- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (BY similarity).			
CC	-!- PATHWAY: Glycolysis.			
CC	-!- SUBUNIT: Homodimer (BY similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- SIMILARITY: Belongs to the enolase family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	EMBL; AF072588; ADD41645.1; -; mRNA.			
DR	HSSP; P56252; 1P0Z.			
DR	SMR; Q9W7L2; 1-A32.			
DR	InterPro; IPR00941; Enolase.			
DR	PANTHER; PTTHR11902; Enolase; 1.			

DR Pfam; PF00113; Enolase\_C; 1.  
DR Pfam; PF03952; Enolase\_N; 1.  
DR PRINTS; PRO0148; ENOLASE; 1.  
DR PRODOM; PD000902; Enolase; 1.  
DR TIGRFAMS; TIGR01060; eno; 1.  
DR PROSITE; PS00164; ENOLASE; 1.  
DR KW GLYCOLYSIS; Lyase; Magnesium; Metal-binding; Multigene family.  
INIT MET 0 By similarity.  
FT METAL 244 Magnesium (By similarity).  
FT METAL 292 Magnesium (By similarity).  
FT METAL 317 Magnesium (By similarity).  
SQ SEQUENCE 433 AA; 47202 MW; 08193329C1D006 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.047;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCITCQIKTGAPC 16  
Db 383 LVVGLCITCQIKTGAPC 398

Search completed: April 3, 2006, 08:03:42  
Job time : 59 secs

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Run on: April 3, 2006, 08:03:55 ; Search time 21 Seconds  
 (without alignment) 62.991 Million cell updates/sec

OM protein - protein search, using sw model.

Title: US-09-647-457F-3

Perfect score: 90

Sequence: 1 LVVGLCTCQIKTGpac 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572050 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*\*  
 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*\*  
 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*\*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*\*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*\*  
 6: /cgn2\_6/ptodata/1/iaa/bactfile1.pep:\*\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	65	72.2	434	2 US-09-949-016-6153 Sequence 6153, Appl
2	65	72.2	443	2 US-09-949-016-8359 Sequence 8359, Appl
3	46	51.1	45	1 US-07-973-852-1 Sequence 1, Appl
4	46	51.1	45	1 US-07-950-773-1 Sequence 1, Appl
5	46	51.1	46	2 US-09-010-619-230 Sequence 230, Appl
6	46	51.1	46	2 US-09-044-281-111 Sequence 111, Appl
7	45	50.0	712	2 US-09-252-991A-20471 Sequence 20471, Appl
8	43	47.8	100	2 US-10-05-901A-51 Sequence 51, Appl
9	43	47.8	452	2 US-09-773-877B-16 Sequence 16, Appl
10	43	47.8	462	2 US-09-773-877B-18 Sequence 18, Appl
11	43	47.8	557	2 US-09-773-877B-14 Sequence 14, Appl
12	43	47.8	567	2 US-09-773-877B-12 Sequence 12, Appl
13	43	47.8	567	2 US-09-773-877B-20 Sequence 20, Appl
14	43	47.8	661	1 US-08-232-530-12 Sequence 12, Appl
15	43	47.8	661	1 US-08-786-16A-12 Sequence 12, Appl
16	43	47.8	687	1 US-08-232-530-6 Sequence 1, Appl
17	43	47.8	687	2 US-08-086-16A-6 Sequence 6, Appl
18	43	47.8	687	2 US-09-227-353-2 Sequence 2, Appl
19	43	47.8	758	1 US-08-874-678-1 Sequence 1, Appl
20	43	47.8	758	1 US-08-433-831-1 Sequence 1, Appl
21	43	47.8	758	2 US-09-551-363-24 Sequence 24, Appl
22	43	47.8	758	2 US-09-348-886-1 Sequence 1, Appl
23	43	47.8	758	2 US-10-05-901A-1 Sequence 6, Appl
24	43	47.8	780	1 US-08-332-538-14 Sequence 2, Appl
25	43	47.8	780	1 US-08-786-16A-14 Sequence 1, Appl
26	43	47.8	911	2 US-09-949-003-425 Sequence 14, Appl
27	43	47.8	1006	2 US-09-949-002-361 Sequence 14, Appl
28	43	47.8	1006	2 US-09-949-002-361 Sequence 1, Appl
29	43	47.8	1311	1 US-08-340-011-5 Sequence 5, Appl
30	43	47.8	1311	2 US-08-901-710-5 Sequence 5, Appl
31	43	47.8	1311	2 US-09-169-079-5 Sequence 5, Appl
32	43	47.8	1338	2 US-08-750-141A-3 Sequence 3, Appl
33	43	47.8	1362	1 US-08-874-678-33 Sequence 6, Appl
34	43	47.8	1362	2 US-08-643-839-33 Sequence 33, Appl
35	43	47.8	1362	2 US-09-348-886-33 Sequence 33, Appl
36	43	47.8	1362	2 US-10-105-901A-33 Sequence 33, Appl
37	43	47.8	1362	2 US-10-087-011-2 Sequence 21129, A
38	43	47.8	1342	2 US-09-248-798A-21129 Sequence 21129, A
39	42	46.7	171	2 US-09-252-991A-21020 Sequence 21020, A
40	42	46.7	444	2 US-09-320-352-7269 Sequence 7269, AP
41	42	46.7	444	2 US-09-540-236-2354 Sequence 2354, AP
42	42	46.7	1101	2 US-09-561-708B-5 Sequence 5, Appl
43	41.5	46.1	1101	2 US-09-561-708B-13 Sequence 13, Appl
44	41.5	46.1	1342	2 US-09-561-708B-13 Sequence 2, Appl
45	41.5	46.1	1342	2 US-09-561-708B-13 Sequence 1, Appl
46	41	45.6	45	1 US-08-84-379-2 Sequence 18, Appl
47	41	45.6	45	1 US-08-495-799-17 Sequence 17, Appl
48	41	45.6	177	2 US-09-227-853A-13 Sequence 17, Appl
49	41	45.6	177	2 US-09-425-794-18 Sequence 13, Appl
50	41	45.6	178	1 US-08-849-232-2 Sequence 18, Appl
51	41	45.6	178	2 US-09-819-813-18 Sequence 18, Appl
52	41	45.6	178	2 US-08-633-191A-4 Sequence 17, Appl
53	40.5	45.0	2556	1 US-08-805-432-17 Sequence 20, Appl
54	40.5	45.0	2556	2 US-08-532-384-20 Sequence 20, Appl
55	40.5	45.0	2556	2 US-08-819-232-2 Sequence 2, Appl
56	40.5	45.0	2556	2 US-09-21-457-2 Sequence 2, Appl
57	40.5	45.0	3084	2 US-09-562-702A-12 Sequence 12, Appl
58	40.5	45.0	3106	2 US-09-662-702A-10 Sequence 10, Appl
59	40.5	45.0	3106	2 US-10-029-217A-24 Sequence 2510, AP
60	40	44.4	300	2 US-09-198-453A-354 Sequence 354, AP
61	40	44.4	300	2 US-09-845-583A-10 Sequence 338, AP
62	40	44.4	341	2 US-09-338-185A-338 Sequence 29179, AP
63	40	44.4	476	2 US-09-552-991A-21179 Sequence 4913, AP
64	40	44.4	891	2 US-09-134-001C-4913 Sequence 1, Appl
65	40	44.4	2211	2 US-09-738-884-1 Sequence 1, Appl
66	40	44.4	2211	2 US-10-096-961A-1 Sequence 1, Appl
67	40	44.4	3907	2 US-10-029-217A-24 Sequence 24, Appl
68	39.5	43.9	1587	2 US-09-845-583A-10 Sequence 10, Appl
69	39.5	43.9	1587	2 US-09-561-709B-3 Sequence 3, Appl
70	39.5	43.9	2523	1 US-08-185-432-18 Sequence 18, Appl
71	39.5	43.9	2523	2 US-08-099-233-3 Sequence 3, Appl
72	39.5	43.9	2523	2 US-09-121-457-3 Sequence 273, AP
73	39	43.3	95	2 US-09-177-249-273 Sequence 273, AP
74	39	43.3	95	2 US-09-812-283-273 Sequence 273, AP
75	39	43.3	115	2 US-09-707-767-42013 Sequence 42013, A
76	39	43.3	121	2 US-09-270-767-3953 Sequence 39953, A
77	39	43.3	121	2 US-09-270-767-553 Sequence 55170, A
78	39	43.3	160	2 US-09-448-96A-17879 Sequence 17879, A
79	39	43.3	180	2 US-09-510-238A-206 Sequence 286, AP
80	39	43.3	272	2 US-09-270-767-3457 Sequence 34757, A
81	39	43.3	272	2 US-09-270-767-49974 Sequence 49974, A
82	39	43.3	384	2 US-09-945-249-8 Sequence 8, Appl
83	39	43.3	384	2 US-09-041-930-8 Sequence 8, Appl
84	39	43.3	481	1 US-07-927-071-1 Sequence 1, Appl
85	39	43.3	516481	1 US-07-927-071-1 Sequence 1, Appl
86	39	43.3	689	2 US-09-77-249-2 Sequence 2, Appl
87	39	43.3	689	2 US-09-61-669A-2 Sequence 2, Appl
88	39	43.3	689	2 US-09-812-283-2 Sequence 2, Appl
89	39	43.3	689	2 US-10-104-07-272 Sequence 2, Appl
90	39	43.3	905	1 US-08-227-439A-1 Sequence 1, Appl
91	39	43.3	932	2 US-10-176-884-15 Sequence 15, Appl
92	39	43.3	992	1 US-08-27-439A-1 Sequence 1, Appl
93	39	43.3	992	1 US-08-82-947-1 Sequence 1, Appl
94	39	43.3	1063	1 US-08-093-453B-3 Sequence 1, Appl
95	39	43.3	1063	1 US-08-227-439A-8 Sequence 1, Appl
96	39	43.3	1063	1 US-08-988-409A-50 Sequence 1, Appl
97	39	43.3	2353	2 US-08-988-409A-50 Sequence 50, AP
98	39	43.3	2732	2 US-08-086-336-30 Sequence 30, AP
99	38.5	42.8	65	6 5177197-51 Patent No. 5177197

## ALIGNMENTS

RESULT 3  
US-07-973-852-1  
; Sequence 1, Application US/07973852  
; Patent No. 537640  
; GENERAL INFORMATION:  
; APPLICANT: Miyazaki, Toshiyuki  
; APPLICANT: Motoi, Hirofumi  
; APPLICANT: Kodama, Toshiaki  
; APPLICANT: Maeda, Tatsuro  
; APPLICANT: Okuda, Hiromichi  
TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS  
NUMBER OF SEQ ID NOS: 7  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIORITY NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-02  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 6153  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6153

RESULT 2  
US-09-949-016-8359  
; Sequence 8359, Application US/09949016  
; Patent No. 681239  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 8359  
LENGTH: 443  
TYPE: PPT  
ORGANISM: Human  
US-09-949-016-8359

Query Match 72.2%; Score 65; DB 2; Length 443;  
Best Local Similarity 81.2%; Pred. No. 0.16;  
Matches 13; Conservatve 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 1  
US-09-949-016-6153  
; Sequence 6153, Application US/09949016  
; Patent No. 681239  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIORITY NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-02  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 6153  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6153

Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.16;  
Matches 13; Conservatve 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 4  
US-07-950-773-1  
; Sequence 1, Application US/07950773  
; Patent No. 5411956  
; GENERAL INFORMATION:  
; APPLICANT: Miyazaki, Toshiyuki

APPLICANT: Motoi, Hirofumi  
 APPLICANT: Kodama, Toshiaki  
 APPLICANT: Maeda, Tatsuro  
 APPLICANT: Tsujita, Takahiro  
 APPLICANT: Okuda, Hiromichi  
 TITLE OF INVENTION: LIPOLYMIC ENZYME INHIBITORS  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBIQON, SPIVAK, MCCLELLAND, MAIER &  
 STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 CITY: Arlington  
 STATE: Virginia  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/950,773  
 FILING DATE: 1990-02-24  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/07/631,321  
 FILING DATE: 20-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OJON, No. 541156mmn F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 1327-003-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 521-4500  
 TELEFAX: (703) 486-2347  
 TELEX: 24855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-950-773-1

RESULT 5  
 Query Match 51.1%; Score 46; DB 1; Length 45;  
 Best Local Similarity 43.8%; Pred. No. 8 8;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 LVVGLCTCQIKTGpac 16  
 Db 24 LcAGvUcrKkissGLsc 39

RESULT 6  
 US-09-44-281-111  
 Sequence 111, Application US/09444281  
 ; Patent No. 6942261  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burian, Jan  
 ; APPLICANT: Bartfeld, Daniel  
 ; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING  
 ; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS  
 ; FILE REFERENCE: 660081.411  
 ; CURRENT APPLICATION NUMBER: US/09/444,281  
 ; CURRENT FILING DATE: 1990-11-19  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 111  
 ; LENGTH: 46  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 ; US-09-444-281-111

RESULT 7  
 US-09-252-991A-20471  
 Sequence 20471, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107156.135  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-27  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; SEQ ID NO 20471  
 ; LENGTH: 712  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-20471

RESULT 8  
 Query Match 50.0%; Score 45; DB 2; Length 712;  
 Best Local Similarity 46.7%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 46.7%; 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 2 VVGLCTCQIKTGpac 16  
 Db 641 VTGSCRNASSSPAC 655

RESULT 9  
 Sequence 230, Application US/09030619B  
 ; Patent No. 6503881  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Krieger, Timothy J.  
 ; APPLICANT: Taylor, Robert  
 ; APPLICANT: Erfile, Douglas  
 ; APPLICANT: Fraser, Janet R.  
 ; APPLICANT: West, Michael H.P.  
 ; APPLICANT: McNicol, Patricia J.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
 ; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
 ; TITLE OF INVENTION: WITH ANTIBIOTICS  
 ; FILE REFERENCE: 660081.406  
 ; CURRENT APPLICATION NUMBER: US/09/030,619B  
 ; CURRENT FILING DATE: 1998-02-25  
 ; NUMBER OF SEQ ID NOS: 232  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 230  
 ; LENGTH: 46  
 ; TYPE: PRT

US-10-105-901A-51  
; Sequence 51, Application US/10105901A  
; Patent No. 639794  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; Chen, Helen H.  
; Prescia, Leonard  
; Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dorsey & Whitney LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/105, 901A  
; FILING DATE: 20-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 09/348, 886  
; FILING DATE: 01-JUL-1999  
; APPLICATION NUMBER: US 08/643, 839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Richard F. Trecartin  
; REGISTRATION NUMBER: 31,801  
; REFERENCE DOCKET NUMBER: A-63291-3/RFT/NBC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEX: (415) 398-3249  
; FAX: 910-277299  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; STRANDEDNESS: unknown  
; TYPE: amino acid  
; MOLECULE TYPE: protein  
; STRANDEDNESS: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
; US-10-105-901A-51  
; Query Match 47.8%; Score 43; DB 2; Length 100;  
; Best Local Similarity 50.0%; Pred. No. 47; Mismatches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
; Matches 1; Indels 0; Gaps 0;  
; QY 4 GLCTCQIKNGPA 15  
; DB 76 GLYTCRVRSGPS 87  
; RESULT 9  
; US-09-773-877B-16  
; Sequence 16, Application US/09773877B  
; Patent No. 633349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT FILING DATE: 2001-01-31  
; CURRENT APPLICATION NUMBER: US/09/773, 877B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 14  
; LENGTH: 557  
; TYPE: PR  
; ORGANISM: Artificial Sequence  
; FEATURE: OTHER INFORMATION: Flt1(1-3 deltaB)-Fc (Mut1)  
; US-09-773-877B-14  
; Query Match 47.8%; Score 43; DB 2; Length 557;  
; Best Local Similarity 50.0%; Pred. No. 2.2e+02; Mismatches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
; Matches 1; Indels 0; Gaps 0;  
; QY 4 GLCTCQIKNGPA 15  
; DB 297 GLYTCRVRSGPS 308  
; SEQ ID NO 16  
; LENGTH: 452  
; TYPE: PR  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1(2-3 deltaB)-Fc  
; US-09-773-877B-16  
; Query Match 47.8%; Score 43; DB 2; Length 452;  
; Best Local Similarity 50.0%; Pred. No. 1.8e+02; Mismatches 5; Conservative 1; Indels 0; Gaps 0;  
; Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

RESULT 12  
US-09-773-877B-12  
; Sequence 12, Application US/09773877B  
; Patent No. 683349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: OTHER INFORMATION: Flt (1-3) -Fc  
; US-09-773-877B-12

Query Match 47.8%; Score 43; DB 2; Length 567;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02; 5; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 13  
US-09-773-877B-20  
; Sequence 20, Application US/09773877B  
; Patent No. 683349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: OTHER INFORMATION: Flt (1-3 R->N) -Fc (Mut4)  
; US-09-773-877B-20

Query Match 47.8%; Score 43; DB 2; Length 567;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02; 5; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15  
Db 281 GLYTCRVRSGPS 292

RESULT 14  
US-08-232-538-12  
; Sequence 12, Application US/08232538  
; Patent No. 5712380  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Kenneth A.  
; APPLICANT: Kendall, Richard L.  
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/786,164  
; FILING DATE: 21-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark Hand, J  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 18888DA  
; TELECOMMUNICATION INFORMATION:  
; TELEFAX: 908-594-4720

RESULT 15  
US-08-786-164-12  
; Sequence 12, Application US/08786164  
; Patent No. 5861484  
; GENERAL INFORMATION:  
; APPLICANT: THOMAS, KENNETH A.  
; APPLICANT: KENDALL, RICHARD L.  
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/786,164  
; FILING DATE: 21-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark Hand, J  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 18888DA  
; TELECOMMUNICATION INFORMATION:  
; TELEFAX: 908-594-4720

RESULT 16  
US-08-232-538-12  
; Sequence 12, Application US/08232538  
; Patent No. 5712380  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Kenneth A.  
; APPLICANT: Kendall, Richard L.  
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STUBEE: P.O. Box 2000, 126 E Lincoln Avenue  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/786,164  
; FILING DATE: 21-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark Hand, J  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 18888DA  
; TELECOMMUNICATION INFORMATION:  
; TELEFAX: 908-594-4720

TABLEX:  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 661 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-786-164-12

Query Match 47.8%; Score 43; DB 1; Length 661;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+02; 5; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 5; Misnmatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15  
 Db 281 GLYTCAVRSGPS 292

RESULT 16  
 US-08-232-538-6  
 Sequence 6, Application US/08232538  
 Patent No. 571280  
 GENERAL INFORMATION:  
 APPLICANT: Thomas, Kenneth A.  
 APPLICANT: Kendall, Richard L.  
 APPLICANT: Kendall, Richard L.  
 TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL GROWTH FACTOR  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck Co., Inc.  
 STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 STATE: NJ  
 CITY: Rahway  
 COUNTRY: USA  
 ZIP: 07065-0900

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Microsoft Word 6.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/786.164  
 FILING DATE: 21-JAN-1997  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICANT NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mark Hand, J  
 REGISTRATION NUMBER: 36,545  
 REFERENCE/DOCKET NUMBER: 18880DA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 908-594-3905  
 TELEFAX: 908-594-4720  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 687 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-786-164-6

Query Match 47.8%; Score 43; DB 1; Length 687;  
 Best Local Similarity 50.0%; Pred. No. 2.7e+02; 5; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 5; Misnmatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15  
 Db 307 GLYTCAVRSGPS 318

RESULT 18  
 US-09-427-353-2  
 Sequence 2, Application US/09427353  
 Patent No. 6375929  
 GENERAL INFORMATION:  
 APPLICANT: THOMAS, KENNETH A.  
 APPLICANT: GOLDMAN, COREY K.  
 APPLICANT: KENDALL, RICHARD L.  
 APPLICANT: BETT, ANDREW J.  
 APPLICANT: HUCKLE, WILLIAM R.  
 TITLE OF INVENTION: GENE THERAPY FOR INHIBITION OF ANGIOGENESIS  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
 STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
 CITY: RAHWAY  
 STATE: NJ  
 ZIP: 07065-0907

COMPUTER READABLE FORM:

RESULT 17  
 US-08-786-164-6  
 Sequence 6, Application US/08786164

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: PASESQ Version 1.5  
 CURRENT APPLICATION NUMBER: US/09/427,353  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 CURRENT APPLICATION DATA:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hand, Mark  
 REGISTRATION NUMBER: 36,545  
 REFERENCE/DOCKET NUMBER: 19810YCA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 731-594-3905  
 TELEFAX: 732-594-4720  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 687 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-09-427-353-2

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 687 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-09-427-353-2

Query Match 47.8%; Score 43; DB 2; Length 687;  
 Best Local Similarity 50.0%; Pred. No. 2.7e+02; Qy 4 GLCTCQIKTGPA 15  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Db 307 GLYTCRVRSGPS 318

RESULT 19  
 US-08-874-678-1  
 Sequence 1, Application US/08874678  
 Patent No. 592199

GENERAL INFORMATION:  
 APPLICANT: Davis-Smyth, Terri L.  
 APPLICANT: Chen, Helen H.  
 APPLICANT: Presta, Leonard H.

APPLICANT: Ferrara, Napoleone  
 TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,839  
 FILING DATE: 07-MAY-1996  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-63291-WHD

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-9899  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 758 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein

US-08-874-678-1

Query Match 47.8%; Score 43; DB 1; Length 758;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+02; Qy 4 GLCTCQIKTGPA 15  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Db 307 GLYTCRVRSGPS 318

RESULT 20  
 US-08-643-839-1  
 Sequence 1, Application US/08643839  
 Patent No. 610071

GENERAL INFORMATION:  
 APPLICANT: Davis-Smyth, Terri L.  
 APPLICANT: Chen, Helen H.  
 APPLICANT: Presta, Leonard H.  
 APPLICANT: Ferrara, Napoleone  
 TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,839  
 FILING DATE: 07-MAY-1996  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-63291-WHD

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-9899  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 758 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein

US-08-643-839-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+02; Qy 4 GLCTCQIKTGPA 15  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCCTCQIKTKGPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 21  
US-09-051-363-24  
Sequence 24, Application US/09051363  
Patent No. 627093  
GENERAL INFORMATION:  
APPLICANT: Shibuya, Masahumi  
APPLICANT: Okamoto, Masaji  
APPLICANT: Niwa, Mikio  
APPLICANT: Matsumoto, Tomoe  
APPLICANT: Asano, Makoto  
APPLICANT: Segawa, Toshiaki  
TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
MEDIUM TYPE: Disquette  
OPERATING SYSTEM: Windows95  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/051,363  
FILING DATE: 07-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/02906  
FILING DATE: 07-OCT-1996  
APPLICATION NUMBER: 8/211892 JP  
FILING DATE: 23-JUL-1996  
APPLICATION NUMBER: 7/296476 JP  
FILING DATE: 07-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Ph.D., J.D., Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 06501/012001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
TOPeOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-051-363-24

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCCTCQIKTKGPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 23  
US-10-105-901A-1  
Sequence 1, Application US/10105901A  
Patent No. 6897294  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flair Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/348,886  
FILING DATE: 01-JUL-1999  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dolly A. Vance  
REGISTRATION NUMBER: 39,054  
REFERENCE/DOCKET NUMBER: A-63291-2/RMS/DAV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPeOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-348-886-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCCTCQIKTKGPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 23  
US-10-105-901A-1  
Sequence 1, Application US/10105901A  
Patent No. 6897294  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dorsey & Whitney LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187

RESULT 22  
US-09-348-886-1  
Sequence 1, Application US/09348886  
Patent No. 6303486  
GENERAL INFORMATION:



RESULT 26 ;  
 US-09-949-002-425 ;  
 ; Sequence 425, Application US/09949002  
 ; Patent No. 6,900016  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: CL0001790  
 ; CURRENT APPLICATION NUMBER: US/09/949,002  
 ; CURRENT FILING DATE: 2000-01-28  
 ; PRIORITY NUMBER: 60/231,401  
 ; PRIORITY FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 10823  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO: 425  
 ; LENGTH: 911  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-002-425

Query Match 47.8%; Score 43; DB 2; Length 911;  
 Best Local Similarity 58.3%; Pred. No. 3.4e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VGGLTCQIKKGP 14  
 Db 365 LNLLTCQVKTNP 376

RESULT 27 ;  
 US-09-023-905A-12 ;  
 ; Sequence 12, Application US/09023905A  
 ; Patent No. 6,475,778  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roberts, Thomas M.  
 ; APPLICANT: King, Frederick J.  
 ; APPLICANT: Harris, David F.  
 ; APPLICANT: Hu, Erding  
 ; APPLICANT: Spiegelman, Bruce  
 ; APPLICANT: Chan, Joanne  
 ; TITLE OF INVENTION: Differentiation Enhancing Factors and Uses  
 ; TITLE OF INVENTION: Therefor  
 ; FILE REFERENCE: DFN-021  
 ; CURRENT APPLICATION NUMBER: US/09/023,905A  
 ; CURRENT FILING DATE: 1998-02-13  
 ; PRIORITY NUMBER: US 60/038,191  
 ; PRIOR FILING DATE: 1997-02-14  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 12  
 ; LENGTH: 106  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-023-905A-12

Query Match 47.8%; Score 43; DB 2; Length 1006;  
 Best Local Similarity 58.3%; Pred. No. 3.8e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VGGLTCQIKKGP 14  
 Db 349 LNLLTCQVKN 360

RESULT 28 ;  
 US-09-949-002-361 ;  
 ; Sequence 361, Application US/09949002  
 ; Patent No. 6,900016  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.

Query Match 47.8%; Score 43; DB 1; Length 1111;  
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
Db ||| : : | : 317 GLYTCRVRSGPS 328

RESULT 30  
US-08-901-710-5  
; Sequence 5 Application US/08901710  
; Patent No. 6107046

Query Match Score 43; DB 2; Length 1311;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
Matches 6; Conservative; Mismatches 1; Indels 0; Gaps 0

Search completed: April 3, 2006, 08:04:25  
Job time : 23 SECs

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; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1043  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-473-127-1043

Query Match 72.2%; Score 65; DB 5; Length 269;  
Best Local Similarity 81.2%; Pred. No. 0.26;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 5  
US-10-473-127-1041  
; Sequence 1041; Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 1043  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Homo sapiens  
; US-10-473-127-1041

Query Match 72.2%; Score 65; DB 5; Length 272;  
Best Local Similarity 81.2%; Pred. No. 0.27;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7  
US-10-473-127-1042  
; Sequence 1042; Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 1042  
LENGTH: 272  
TYPE: PRT  
ORGANISM: Homo sapiens  
; US-10-473-127-1042

Query Match 72.2%; Score 65; DB 5; Length 336;  
Best Local Similarity 81.2%; Pred. No. 0.32;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 6

Qy

1 LVNGLCCTCQIKTGPC 16  
Db 222 LVNGLCCTCQIKTGPC 237

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Db      286 LVVGLCTQIKTGAPC 301
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 604
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-604

Query Match          72.2%; Score 65; DB 5; Length 429;
Best Local Similarity 81.2%; Pred. No. 0.4%; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Organsim Homo sapiens
; Sequence 9, Application US/09935642
; Publication No. US0030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRAJSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human
; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-642-9

Query Match          72.2%; Score 65; DB 3; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.41%; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Organsim Homo sapiens
; Sequence 61, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; US-10-473-127-604
; Sequence 604, Application US/10473127
; GENERAL INFORMATION:
; APPLICANT: ZYCOB INC.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-036W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; RESULT 9
; US-10-473-127-604
; Publication No. US20040236091A1
; Sequence 604, Application US/10473127
; GENERAL INFORMATION:
; APPLICANT: Lee, Soo Yean
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Lee, Brnesine A.
; APPLICANT: Khare, Reena
; APPLICANT: Tran, Uyen K.
; APPLICANT: Kable, Amy E.
; APPLICANT: Richardson, Thomas W.
; APPLICANT: Emerling, Brooke M.
; APPLICANT: Lindquist, Erika A.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hafalia, April J. A.
; APPLICANT: Li, Joana X.
; APPLICANT: Marquis, Joseph P.
; APPLICANT: Lee, Sally
; APPLICANT: Gorvad, Ann E.
; APPLICANT: Sprague, William W.
; APPLICANT: Becha, Shanya D.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PP-1112 PCT
; CURRENT APPLICATION NUMBER: US/10/498,788
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,962
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/343,558
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/351,107
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PERL Program
; SEQ ID NO: 17
; LENGTH: 420
; TYPE: PRT
; FEATURE:
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506054CD1
; US-10-498-788-17

Query Match          72.2%; Score 65; DB 5; Length 420;
Best Local Similarity 81.2%; Pred. No. 0.39%; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Organsim Homo sapiens
; Sequence 1, LVVGLCTQIKTGAPC 16
; Publication No. US20040236091A1
; Sequence 370, LVVGLCTQIKTGAPC 385
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-642-9

Query Match          72.2%; Score 65; DB 3; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.41%; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Organsim Homo sapiens
; Sequence 1, LVVGLCTQIKTGAPC 16
; Publication No. US20040219572A1
; Sequence 383, LVVGLCTQIKTGAPC 398
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-73-969A-61
; Sequence 61, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; RESULT 11
; US-10-73-969A-61
; Sequence 61, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING

```

APPLICANT: LIU, TONG HUA  
 APPLICANT: SHEN, YAN  
 TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER  
 FILE REFERENCE: 21525  
 CURRENT APPLICATION NUMBER: US/10/733, 969A  
 CURRENT FILING DATE: 2003-12-11  
 PRIORITY APPLICATION NUMBER: EP 02028058.2  
 PRIORITY FILING DATE: 2002-12-17  
 NUMBER OF SEQ ID NOS: 110  
 SOFTWARE: Patentin version 3.2  
 SEQ ID NO: 61  
 LENGTH: 433  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: human alpha enolase; Accession NO:  
 US-10-733-969A-61

Query Match 72.2%; Score 65; DB 5; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.41; 3; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVNGLCTCQIKTGPC 16  
 Db 383 LVNGLCTCQIKTGPC 398

RESULT 12  
 Sequence 608, Application US/10/73127  
 GENERAL INFORMATION:  
 Publication No. US20040236091A1  
 APPLICANT: Zycos Inc.  
 TITLE OF INVENTION: TRANSLATIONAL PROFILING  
 FILE REFERENCE: 08191-026701  
 CURRENT APPLICATION NUMBER: US/10/473, 127  
 PRIORITY APPLICATION NUMBER: 60/279, 495  
 PRIORITY FILING DATE: 2001-03-28  
 PRIORITY APPLICATION NUMBER: 60/292, 544  
 PRIORITY FILING DATE: 2001-05-21  
 PRIORITY APPLICATION NUMBER: 60/310, 801.  
 PRIORITY FILING DATE: 2001-08-08  
 PRIORITY APPLICATION NUMBER: 60/326, 370  
 PRIORITY FILING DATE: 2001-10-01  
 PRIORITY APPLICATION NUMBER: 60/336, 780  
 PRIORITY FILING DATE: 2001-12-04  
 PRIORITY APPLICATION NUMBER: 60/358, 985  
 PRIORITY FILING DATE: 2002-02-20  
 NUMBER OF SEQ ID NOS: 2041  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 608  
 LENGTH: 433  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-473-127-608

Query Match 72.2%; Score 65; DB 5; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.41; 3; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVNGLCTCQIKTGPC 16  
 Db 383 LVNGLCTCQIKTGPC 398

RESULT 14  
 Sequence 124, Application US/10177293  
 Publication No. US20030124128A1  
 GENERAL INFORMATION:  
 APPLICANT: Billie, James  
 APPLICANT: Glatt, Karen  
 APPLICANT: Zhao, Xumei  
 APPLICANT: Gammavarpi, Manjula  
 APPLICANT: Kamatkar, Shubhangi  
 APPLICANT: Mertens, Maureen  
 APPLICANT: Myer, Vic  
 APPLICANT: Wang, Youzhen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Hoersch, Sebastian  
 APPLICANT: Monahan, John  
 APPLICANT: Meyers, Rachel E.  
 APPLICANT: Bast Jr., Robert C.  
 APPLICANT: Horrobagyi, Gabriel N.  
 APPLICANT: Pusztai, Lajos  
 APPLICANT: Meric, Funda  
 APPLICANT: Sahin, Aysegul  
 APPLICANT: Millis, Gordon B.  
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT  
 FILE REFERENCE: MRI-018  
 CURRENT APPLICATION NUMBER: US/10/177, 293  
 CURRENT FILING DATE: 2003-06-21  
 PRIORITY APPLICATION NUMBER: US 60/299, 887  
 PRIORITY FILING DATE: 2001-06-21  
 PRIORITY APPLICATION NUMBER: US 60/301, 572  
 PRIORITY FILING DATE: 2001-06-27  
 PRIORITY APPLICATION NUMBER: US 60/306, 501  
 PRIORITY FILING DATE: 2001-07-18  
 PRIORITY APPLICATION NUMBER: US 60/325, 002  
 PRIORITY FILING DATE: 2001-09-25  
 PRIORITY APPLICATION NUMBER: US 60/362, 585  
 PRIORITY FILING DATE: 2002-03-05  
 PRIORITY APPLICATION NUMBER: US 60/xxxx, xxxx

RESULT 13  
 Query Match 72.2%; Score 65; DB 5; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.41; 3; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVNGLCTCQIKTGPC 16  
 Db 383 LVNGLCTCQIKTGPC 398

RESULT 13  
 Sequence 610, Application US/10473127  
 Publication No. US20040236091A1  
 GENERAL INFORMATION:

PRIOR FILING DATE: 2002-05-14 ;  
; NUMBER OF SEQ ID NOS: 506 ;  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 124  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-177-293-124

RESULT 15  
Query Match Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

US-10-205-194-47  
Query Match Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

RESULT 16  
Query Match Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

US-10-205-194-47  
; CURRENT APPLICATION NUMBER: US/10/205,194  
; CURRENT FILING DATE: 5/20/02-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 47  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Neuron-specific enolase  
; US-10-205-194-47

RESULT 17  
US-10-354-358-16  
Query Match Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

US-10-354-358-16  
; CURRENT APPLICATION NUMBER: US/10/354,358  
; CURRENT FILING DATE: 5/20/02-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 16  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-354-358-16

RESULT 17  
US-10-170-385-257  
Query Match Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 3; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

US-10-170-385-257  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 5/20/02-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; NUMBER OF SEQ ID NOS: 549  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 257  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-10-170-385-257

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 18  
US-10-170-385-273  
Sequence 273, Application US/10170385  
Publication No. US20030203372A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Neil Raymond  
APPLICANT: Mundy, Christopher Robert  
APPLICANT: Kan, On  
APPLICANT: Harris, Robert Alan  
APPLICANT: White, Jonathan  
APPLICANT: Binley, Katie Mary  
APPLICANT: Rayner, William Nigel  
APPLICANT: Naylor, Stuart  
APPLICANT: Kingsman, Susan Mary  
APPLICANT: Krige, David  
TITLE OF INVENTION: ANALYSIS METHOD  
FILE REFERENCE: S32682000100  
CURRENT APPLICATION NUMBER: US/10/170,385  
CURRENT FILING DATE: 2002-06-12  
PRIORITY APPLICATION NUMBER: PCT/GB02/01662  
PRIORITY FILING DATE: 2002-04-08  
PRIORITY APPLICATION NUMBER: PCT/GB01/05458  
PRIORITY FILING DATE: 2001-12-10  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 273  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-170-385-273

RESULT 19  
US-10-258-666-10  
Sequence 10, Application US/10258666  
Publication No. US20040005578A1  
GENERAL INFORMATION:  
APPLICANT: Yamada, Yoji  
APPLICANT: Sakine, Subumu  
APPLICANT: Kikuchi, Yasuhiro  
APPLICANT: Sakurada, Kazuhiko  
APPLICANT: Kyowa Hakko Kogyo Co., Ltd.  
TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes  
FILE REFERENCE: 082382-00000US  
CURRENT APPLICATION NUMBER: US/10/258,666  
CURRENT FILING DATE: 2003-05-23  
PRIORITY APPLICATION NUMBER: JP 2000-126741  
PRIORITY FILING DATE: 2000-04-27  
PRIORITY APPLICATION NUMBER: WO PCT/JP01/03700  
PRIORITY FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Rattus norvegicus

FEATURE:  
OTHER INFORMATION: RHDH-099, non-neuronal enolase  
US-10-258-666-10

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 20  
US-10-205-331-26  
Sequence 26, Application US/10205331  
Publication No. US2004005836A1  
GENERAL INFORMATION:  
APPLICANT: Warner-Lambert Company  
APPLICANT: Lee, Kevin  
APPLICANT: Dixon, Alastair  
APPLICANT: Brookbank, Robert  
APPLICANT: Pincock, Robert  
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
FILE REFERENCE: WI-A-018199  
CURRENT APPLICATION NUMBER: US/10/205,331  
CURRENT FILING DATE: 2002-07-24  
PRIORITY APPLICATION NUMBER: GB 0118354.0  
PRIORITY FILING DATE: 2001-07-27  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Alpha-enolase  
US-10-205-331-26

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 21  
US-10-473-127-595  
Sequence 595, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: ZYCOs, INC.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIORITY APPLICATION NUMBER: 60/279,495  
PRIORITY FILING DATE: 2001-03-28  
PRIORITY APPLICATION NUMBER: 60/292,544  
PRIORITY FILING DATE: 2001-05-21  
PRIORITY APPLICATION NUMBER: 60/310,801  
PRIORITY FILING DATE: 2001-08-08  
PRIORITY APPLICATION NUMBER: 60/326,370  
PRIORITY FILING DATE: 2001-10-01  
PRIORITY APPLICATION NUMBER: 60/336,780  
PRIORITY FILING DATE: 2001-12-04  
PRIORITY APPLICATION NUMBER: 60/358,985  
PRIORITY FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 595  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 595

LENGTH: 434 ;  
; TYPE: PRT ;  
; ORGANISM: Homo sapiens ;  
; US-10-473-127-595 ;  
; Query Match 72.2%; Score 65; DB 5; Length 434;  
; Best Local Similarity 81.2%; Pred. No. 0.41; ;  
; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
; Qy 1 LVVGLCTCQIKTGAC 16  
; Db 384 LVVGLCTCQIKTGAC 399

RESULT 22  
US-10-473-127-596  
; Sequence 596, Application US/10473127  
; Publication No. US2004026091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 596  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-473-127-596

Query Match 72.2%; Score 65; DB 5; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; ;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

RESULT 23  
US-10-473-127-597  
; Sequence 597, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 598  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-473-127-598

Query Match 72.2%; Score 65; DB 5; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; ;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

RESULT 24  
US-10-473-127-598  
; Sequence 598, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 598  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-473-127-598

Query Match 72.2%; Score 65; DB 5; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41; ;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 LVVGLCTCQIKTGAC 16  
Db 384 LVVGLCTCQIKTGAC 399

RESULT 25  
US-10-473-127-599  
; Sequence 599, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/310,801

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; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/3326, 370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/3336, 780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/3358, 985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2141
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 599
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-599

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Query Match          72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;
Qy      1 LVVGLCTCQIKTGAPC 16
Db      384 LVVGLCTCQIKTGAPC 399

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RESULT 26

US-10-473-127-600

Sequence 600, Application US/10473127

Publication No. US20040236091A1

GENERAL INFORMATION:

APPLICANT: Zycos Inc.

TITLE OF INVENTION: TRANSLATIONAL PROFILING

FILE REFERENCE: 08191-026W01

CURRENT APPLICATION NUMBER: US/10/473, 127

PRIORITY FILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: 60/279, 495

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: 60/292, 544

PRIOR FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 60/310, 801

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/326, 370

PRIOR FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: 60/336, 780

PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 60/358, 985

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 2041

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 600

LENGTH: 434

TYPE: PRT

ORGANISM: Homo sapiens

; US-10-473-127-601

; PRIOR APPLICATION NUMBER: 60/279, 495

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292, 544

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: 60/310, 801

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326, 370

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336, 780

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358, 985

; PRIOR FILING DATE: 2002-02-20

; NUMBER OF SEQ ID NOS: 2041

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO: 602

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-473-127-602

; Query Match 72.2%; Score 65; DB 5; Length 434;

; Best Local Similarity 81.2%; Pred. No. 0.41; 3; Indels 0; Gaps 0;

; Matches 13; Conservative 0; Mismatches 0; Gaps 0;

; Qy 1 LVVGLCTCQIKTGAPC 16

; Db 384 LVVGLCTCQIKTGAPC 399

; RESULT 27

; US-10-473-127-601

; Sequence 601, Application US/10473127

; Publication No. US20040236091A1

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: TRANSLATIONAL PROFILING

; FILE REFERENCE: 08191-026W01

; CURRENT APPLICATION NUMBER: US/10/473, 127

; PRIOR FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/279, 495

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292, 544

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: 60/310, 801

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326, 370

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336, 780

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358, 985

; PRIOR FILING DATE: 2002-02-20

; NUMBER OF SEQ ID NOS: 2041

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO: 602

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-473-127-603

; Sequence 603, Application US/10473127

; Publication No. US20040236091A1

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: TRANSLATIONAL PROFILING

; FILE REFERENCE: 08191-026W01

; CURRENT APPLICATION NUMBER: US/10/473, 127

; PRIOR FILING DATE: 2003-09-26

Search completed: April 3, 2006, 08:17:02  
 Job time : 168 sec

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; APPLICANT: ZYCOB Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-11-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SEQ ID NO 603
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-603

RESULT 30
US-10-473-127-609
Query Match 72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVVGLCTCQIKTGAC 16
Db 384 LVVGLCTGQIKTGAPC 399

; Sequence 609, Application US/10/73127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOB Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 609
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-609

Query Match 72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVVGLCTCQIKTGAC 16
Db 384 LVVGLCTGQIKTGAPC 399

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GenCore version 5.1.7

Run on: April 3, 2006, 08:07:10 ; Search time 12 Seconds  
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**Title:** US-009-647-457F-3

**Perfect Score:** 90

**Sequence:** I L V G L C T Q I K T G P A C 16

**Scoring table:** BLOSUM62

**Gapop 10.0 , Gapext 0.5**

**Searched:** 180808 seqs, 34441898 residues

**Total number of hits satisfying chosen parameters:** 180808

**Minimum DB Seq length:** 0

**Maximum DB Seq length:** 200000000

**Post-processing:** Minimum Match 0%

**Maximum Match 100%**

**Listing first 100 summaries**

**Database :**

**Published Applications AA New,\***

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**SUMMARIES**

**Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.**

**Result No.**   **Score**   **Query Length**   **DB ID**   **Description**

Result No.	Score	Query Length	DB ID	Description
1	74	82.2	458	6 US-10-878-556A-28
2	65	72.2	434	6 US-10-878-556A-28
3	65	72.2	434	7 US-11-682-234-153
4	47.5	52.8	1620	6 US-10-055-877-213
5	47.5	52.8	1664	6 US-10-055-877-212
6	46	51.1	46	7 US-11-068-783-111
7	45.5	50.6	127	7 US-11-172-740-2156
8	43	47.8	100	7 US-11-013-693-51
9	43	47.8	452	7 US-11-016-503-6
10	43	47.8	462	7 US-11-016-503-8
11	43	47.8	557	7 US-11-016-503-4
12	43	47.8	567	7 US-11-016-503-2
13	43	47.8	567	7 US-11-016-503-10
14	43	47.8	758	7 US-11-013-693-1
15	43	47.8	1338	6 US-10-821-234-1622
16	43	47.8	1338	7 US-11-019-156-23
17	43	47.8	1338	7 US-11-075-047-A2
18	43	47.8	1362	7 US-11-013-693-33
19	42	46.7	296	7 US-11-012-343-31
20	42	46.7	360	7 US-11-112-240-1
21	42	46.7	360	7 US-11-112-304-1
22	42	46.7	544	6 US-10-990-388-40
23	41	45.6	839	7 US-11-056-562A-24462
24	41	45.6	878	7 US-11-056-562A-24461
25	41	45.6	909	7 US-11-056-562A-24460

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Sequence 2510, Ap  
Sequence 3, Appli  
Sequence 12, Appli  
Sequence 18, Appli  
Sequence 6, Appli  
Sequence 20, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 51, Appli  
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Sequence 8, Appli  
Sequence 2728, Ap  
Sequence 1045, Ap  
Sequence 211, App  
Sequence 55, Appli  
Sequence 6, Appli  
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Sequence 1015, Ap  
Sequence 1076, Ap  
Sequence 30, Appli  
Sequence 6, Appli  
Sequence 9458, Ap  
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Sequence 6, Appli  
Sequence 4, Appli  
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Sequence 78, Appli  
Sequence 38, Appli  
Sequence 72, Appli  
Sequence 66, Appli  
Sequence 214, App  
Sequence 212, App  
Sequence 220, App  
Sequence 72, Appli  
Sequence 232, App  
Sequence 38, Appli  
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Sequence 884, App  
Sequence 860, App



PRIOR APPLICATION NUMBER: 60/263, 799  
 PRIOR FILING DATE: 2001-01-24  
 PRIOR APPLICATION NUMBER: 60/264, 117  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 60/264, 139  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 60/264, 478  
 PRIOR FILING DATE: 2001-01-26  
 PRIOR APPLICATION NUMBER: 60/263, 351  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: 60/272, 870  
 PRIOR FILING DATE: 2001-03-02  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 213  
 LENGTH: 1620  
 TYPE: PRT  
 ORGANISM: *Caenorhabditis elegans*  
 US-10-055-877-213

Query Match 52.8%; Score 47.5; DB 6; Length 1620;  
 Best Local Similarity 62.5%; Pred. No. 9; 2; Mismatches 5; Indels 1; Gaps 1;  
 Matches 10; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	Db
2 VVGLCTC-QIKTGAC 16	876 VIGTCCTCLPGKTPGLC 891

RESULT 5  
 US-10-055-877-212

Sequence 212, Application US1/005877  
 Publication No. US20050288241A1

GENERAL INFORMATION:  
 APPLICANT: Decrisofaro, Marc  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Miller, Charles  
 APPLICANT: Tchernov, Velizar  
 APPLICANT: Zhong, Mei  
 APPLICANT: Anderson, David  
 APPLICANT: Ballinger, Robert  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Spytek, Kimberly  
 APPLICANT: Ratelli, Luca  
 APPLICANT: Kekuda, Ramesh  
 APPLICANT: Guo, Xiaojia  
 APPLICANT: Zerhouni, Bryan  
 APPLICANT: Andrew, David  
 APPLICANT: Mezes, Peter  
 APPLICANT: Paturajan, Meera  
 APPLICANT: Burgess, Catherine  
 APPLICANT: Eisen, Andrew  
 APPLICANT: Wolenc, Adam  
 APPLICANT: Baumgartner, Jason  
 APPLICANT: Shirkets, Richard  
 APPLICANT: Gusev, Vladimir  
 APPLICANT: Vernet, Corine  
 APPLICANT: Taupier Jr., Raymond  
 APPLICANT: Pena, Carol  
 APPLICANT: Shenoy, Suresh  
 APPLICANT: Li, Li  
 APPLICANT: Casman, Stacie  
 APPLICANT: Boldog, Ference

FILE REFERENCE: 21402-251  
 FILE REFERENCE: 21402-251  
 CURRENT APPLICATION NUMBER: US1/0055, 877  
 CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: 60/263, 598  
 PRIOR FILING DATE: 2001-01-23  
 PRIOR APPLICATION NUMBER: 60/263, 799  
 PRIOR FILING DATE: 2001-01-24  
 PRIOR APPLICATION NUMBER: 60/264, 117  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 60/264, 139  
 PRIOR FILING DATE: 2001-01-26  
 PRIOR APPLICATION NUMBER: 60/263, 351  
 PRIOR FILING DATE: 2001-01-27  
 PRIOR APPLICATION NUMBER: 60/272, 870  
 PRIOR FILING DATE: 2001-03-02  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 512

PRIOR APPLICATION NUMBER: 60/275, 990  
 PRIOR FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: 60/275, 927  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 512

PRIOR APPLICATION NUMBER: 60/275, 927  
 PRIOR FILING DATE: 2001-03-14  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 212  
 LENGTH: 1664  
 TYPE: PRT  
 ORGANISM: *Caenorhabditis elegans*  
 US-10-055-877-212

Query Match 52.8%; Score 47.5; DB 6; Length 1664;  
 Best Local Similarity 62.5%; Pred. No. 9; 4; Mismatches 5; Indels 1; Gaps 1;  
 Matches 10; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	Db
2 VVGLCTC-QIKTGAC 16	828 VIGTCCTCLPGKTPGLC 843

RESULT 6  
 US-11-068-783-111

Sequence 111, Application US/11068783  
 Publication No. US20050260715A1

GENERAL INFORMATION:  
 APPLICANT: Burian, Jan  
 APPLICANT: Bartfeld, Daniel  
 TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING  
 TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS  
 CURRENT APPLICATION NUMBER: US/11/068, 783  
 CURRENT FILING DATE: 2005-02-28  
 PRIOR APPLICATION NUMBER: US/09/444,281  
 NUMBER OF SEQ ID NOS: 113  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 111  
 LENGTH: 46  
 TYPE: PRT  
 ORGANISM: *Hordeum vulgare*  
 US-11-068-783-111

Query Match 51.1%; Score 46; DB 7; Length 46;  
 Best Local Similarity 53.8%; Pred. No. 0.67; Mismatches 4; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	Db
4 GLCTCQIKTGAC 16	28 GACRCKISGPK 40

RESULT 7  
 US-11-172-740-2156  
 ; Sequence 2156, Application US/11172740  
 ; Publication No. US2006057774A1  
 ; GENERAL INFORMATION:

APPLICANT: MASCIA, Peter  
 APPLICANT: ALEXANDROV, Nicolai  
 APPLICANT: BROVER, Vrachislav  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR  
 FILE REFERENCE: 2750-160-PBPS2  
 CURRENT APPLICATION NUMBER: US/11/172,740  
 PRIOR FILING DATE: 2005-06-30  
 PRIOR APPLICATION NUMBER: 60/583,621  
 PRIORITY FILING DATE: 2004-06-30  
 PRIOR APPLICATION NUMBER: 60/584,829  
 PRIOR FILING DATE: 2004-06-30  
 PRIOR APPLICATION NUMBER: 60/584,800  
 PRIOR FILING DATE: 2004-06-30  
 NUMBER OF SEQ ID NOS: 2523  
 SEQ ID NO: 2156  
 LENGTH: 127  
 TYPE: PRT  
 ORGANISM: Arabidopsis thaliana  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(127)  
 OTHER INFORMATION: Public GI no. 46396244  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION:  
 OTHER INFORMATION: Utility: Useful for making smaller plants  
 US-11-172-740-2156

Query Match 50.6%; Score 45.5; DB 7; Length 127;  
 Best Local Similarity 47.4%; Pred. No. 2; Mismatches 9; Conservative 3; Indels 5; Gaps 1;  
 Matches 2; Qy 3 VGLC---TCQIKTGpac 16  
 Db 33 LGICETCDERCOAHRGpSc 51

RESULT 8  
 US-11-043-693-51  
 ; Sequence 51, Application US/11043693  
 ; Publication No. US2005021831A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis-Smyth, Terri L.  
 ; APPLICANT: Chen, Helen H.  
 ; APPLICANT: Presta, Leonard  
 ; APPLICANT: Ferrara, Napoleone  
 ; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dorsey & Whitney LLP  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/11/043,693

Query Match 47.8%; Score 43; DB 7; Length 452;  
 Best Local Similarity 50.0%; Pred. No. 15; Mismatches 6; Conservative 5; Indels 1; Gaps 0; Gaps 0;  
 Matches 6; Qy 4 GLCTCQIKGpA 15  
 Db 192 GLYTCRVRSGPS 203

RESULT 9  
 US-11-16-503-6  
 ; Sequence 6, Application US/11016503  
 ; Publication No. US2005024547A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas J. Papadopoulos et al.  
 ; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING THEREOF  
 ; TITLE OF INVENTION: AND USING THEREOF  
 ; FILE REFERENCE: REG 710-A-US  
 ; CURRENT APPLICATION NUMBER: US/11/016,503  
 ; PRIOR APPLICATION NUMBER: US/10/009,852  
 ; PRIOR FILING DATE: 2001-12-06  
 ; CURRENT FILING DATE: 2004-12-17  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/138,133  
 ; PRIOR FILING DATE: 1999-06-08  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 452  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-16-503-6

Query Match 47.8%; Score 43; DB 7; Length 452;  
 Best Local Similarity 50.0%; Pred. No. 15; Mismatches 6; Conservative 5; Indels 1; Gaps 0; Gaps 0;  
 Matches 6; Qy 4 GLCTCQIKGpA 15  
 Db 192 GLYTCRVRSGPS 203

RESULT 10  
 US-11-016-503-8  
 ; Sequence 8, Application US/11016503

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; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIORITY APPLICATION NUMBER: US/10/009,852
; PRIORITY FILING DATE: 2001-12-06
; PRIORITY APPLICATION NUMBER: PCT/US00/14142
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY APPLICATION NUMBER: 60/138,133
; PRIORITY FILING DATE: 1999-06-08
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-8
; Query Match
; Best Local Similarity 50.0%; Pred. No. 16; Length 462;
; Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
; Qy 4 GLTCQKTKGPA 15
; Db 202 GLYTCRVRSGPS 213
; RESULT 11
; US-11-016-503-4
; Sequence 4, Application US/11/016503
; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; Publication No. US2005024547A1
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIORITY APPLICATION NUMBER: US/10/009,852
; PRIORITY FILING DATE: 2001-12-06
; PRIORITY APPLICATION NUMBER: PCT/US00/14142
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY FILING DATE: 1999-06-08
; PRIORITY FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-4
; Query Match
; Best Local Similarity 50.0%; Pred. No. 19; Length 557;
; Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
; Qy 4 GLTCQKTKGPA 15
; Db 297 GLYTCRVRSGPS 308
; RESULT 12
; US-11-016-503-2
; Sequence 2, Application US/11/016503
; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Prasta, Leonard
; APPLICANT: Chen, Helen H.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: David-Smyth, Terri L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Nicholas J. Papadopoulos et al.

RESULT 12
US-11-016-503-2
; Sequence 2, Application US/11/016503
; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Prasta, Leonard
; APPLICANT: Chen, Helen H.
; APPLICANT: David-Smyth, Terri L.
; APPLICANT: Nicholas J. Papadopoulos et al.

RESULT 13
US-11-016-503-10
; Sequence 10, Application US/11/016503
; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIORITY APPLICATION NUMBER: US/10/009,852
; PRIORITY FILING DATE: 2001-12-06
; PRIORITY APPLICATION NUMBER: PCT/US00/14142
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY APPLICATION NUMBER: 60/138,133
; PRIORITY FILING DATE: 1999-06-08
; PRIORITY FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-10
; Query Match
; Best Local Similarity 50.0%; Pred. No. 19; Length 567;
; Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
; Qy 4 GLTCQKTKGPA 15
; Db 307 GLYTCRVRSGPS 318
; RESULT 14
; US-11-043-693-1
; Sequence 1, Application US/11043693
; Publication No. US20050281831A1
; GENERAL INFORMATION:
; APPLICANT: David-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Prasta, Leonard
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Nicholas J. Papadopoulos et al.

RESULT 14
US-11-043-693-1
Sequence 1, Application US/11043693
Publication No. US20050281831A1
GENERAL INFORMATION:
APPLICANT: David-Smyth, Terri L.
APPLICANT: Chen, Helen H.
APPLICANT: Prasta, Leonard
APPLICANT: Ferrara, Napoleone
APPLICANT: Nicholas J. Papadopoulos et al.

```

TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/043,693

FILING DATE: 26-Jan-2005

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/105,901

FILING DATE: 20-Mar-2002

APPLICATION NUMBER: 09/348,886

FILING DATE: 01-JUL-1999

APPLICATION NUMBER: US 08/643,839

FILING DATE: 07-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Richard F. Trecartin

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1985

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 758 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-11-043-693-1

RESULT 16 ; ORGANISM: Homo sapiens  
US-10-821-234-1622  
Query Match ; Sequence 23, Application US/11/09156  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Toshio Ota  
APPLICANT: Tokao Isogai  
APPLICANT: Tetsuo Nishikawa  
APPLICANT: Koji Hayashi  
APPLICANT: Kaoru Otsuka  
APPLICANT: Jun-Ichi Yamamoto  
APPLICANT: Shizuko Ishii  
APPLICANT: Tomoyasu Sugiyama  
APPLICANT: Ai Wakamatsu  
APPLICANT: Keiichi Nagai  
APPLICANT: Tetsuji Funahashi  
APPLICANT: Chiaki Senoo  
APPLICANT: Jun-ichi Nezu  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN FILE REFERENCE: 06501-099002  
CURRENT APPLICATION NUMBER: US/11/109,156  
PRIORITY FILING DATE: 2005-04-19  
PRIORITY APPLICATION NUMBER: US/10/060,065  
PRIORITY FILING DATE: 2002-01-29  
PRIORITY APPLICATION NUMBER: PCT/JP00/05061  
PRIORITY FILING DATE: 2000-07-28  
PRIORITY APPLICATION NUMBER: US 60/159,590  
PRIORITY FILING DATE: 1999-10-18  
PRIORITY APPLICATION NUMBER: US 60/183,322  
PRIORITY FILING DATE: 2000-02-17  
PRIORITY APPLICATION NUMBER: JP 11-248036  
PRIORITY FILING DATE: 1999-07-29  
PRIORITY APPLICATION NUMBER: JP 2000-118776  
PRIORITY FILING DATE: 2000-01-11  
PRIORITY APPLICATION NUMBER: JP 2000-183767  
PRIORITY FILING DATE: 2000-05-02  
PRIORITY APPLICATION NUMBER: JP 2000-241899  
PRIORITY FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS.: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 23  
LENGTH: 1338  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-109-156-23

Query Match ; Sequence 2, Application US/11/075047A  
Best Local Similarity 47.8%; Score 43; DB 7; Length 1338;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCRCQIKKGPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 17 ; ORGANISM: Homo sapiens  
US-11-075-047A-2  
Query Match ; Sequence 2, Application US/11/075047A  
Publication No. US20060030000A1

; GENERAL INFORMATION:  
; APPLICANT: ALITALO, et al.  
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS  
; FILE REFERENCE: 2897/39700A  
; CURRENT APPLICATION NUMBER: US/11/075,047A  
; PRIORITY FILING DATE: 2004-03-07  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 1338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-075-047A-2

RESULT 18  
US-11-043-693-33  
; Sequence 33, Application US/11043693  
; Publication No. US20050281831A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presa, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL PROTEIN INVENTION: PRODUCTION  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Doreen & Whitney LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/043,693  
; FILING DATE: 26-Jan-2005  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/10/105,901  
; FILING DATE: 20-Mar-2002  
; APPLICATION NUMBER: 09/348,886  
; FILING DATE: 01-Jul-1999  
; APPLICATION NUMBER: US 08/643,839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Richard F. Trecatin  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1362 amino acids  
; TYPE: amino acid

RESULT 19  
US-11-182-343-31  
; Sequence 31, Application US/11182343  
; Publication No. US20060018910A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce  
; APPLICANT: Gualberto, Antonio  
; APPLICANT: Melvin, Carrie  
; APPLICANT: Roberts, Luisa M.  
; TITLE OF INVENTION: COMBINANT TREATMENT FOR BREAST CANCER  
; FILE REFERENCE: PC3226A  
; CURRENT APPLICATION NUMBER: US/11/182,343  
; CURRENT FILING DATE: 2005-07-15  
; PRIORITY FILING DATE: 2004-07-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 31  
; LENGTH: 296  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-182-343-31

RESULT 20  
US-11-112-240-1  
; Sequence 1, Application US/11112240  
; Publication No. US20050287140A1  
; GENERAL INFORMATION:  
; APPLICANT: Smothers, James F.  
; APPLICANT: Fanslow III, William C.  
; APPLICANT: Kariv, Revital  
; TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148  
; FILE REFERENCE: A-953A(US)  
; CURRENT APPLICATION NUMBER: US/11/112,240  
; CURRENT FILING DATE: 2005-04-21  
; PRIORITY APPLICATION NUMBER: US 60/564,885  
; PRIORITY FILING DATE: 2004-04-23  
; PRIORITY APPLICATION NUMBER: US 60/585,885  
; PRIORITY FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-112-240-1

Query Match Best Local Similarity 46.7%; Score 42; DB 7; Length 360;  
Matches 7; Conservative 53.8%; Pred. No. 18; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPAC 16 ;  
Db 56 GACTCCCTGTGC 68 ; PRIOR FILING DATE: 2000-02-23  
; Sequence 1, Application US/11112304A ; PRIOR APPLICATION NUMBER: 60/188, 880  
; Publication No. US2006002931A1 ; PRIOR FILING DATE: 2000-03-13  
; GENERAL INFORMATION: ; PRIOR APPLICATION NUMBER: 60/217, 369  
; APPLICANT: AMGEN, INC. ; PRIOR FILING DATE: 2000-07-11  
; APPLICANT: Smothers, James ; PRIOR APPLICATION NUMBER: 60/217, 370  
; APPLICANT: Kariy, Revital ; PRIOR FILING DATE: 2000-07-11  
; TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; FILE REFERENCE: 3447 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; CURRENT APPLICATION NUMBER: US/11/112, 304A ; PRIOR APPLICATION NUMBER: 60/217, 370  
; CURRENT FILING DATE: 2005-04-22 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; PRIOR APPLICATION NUMBER: US 60/565, 158 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; PRIOR FILING DATE: 2004-04-23 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; PRIOR APPLICATION NUMBER: US 60/564, 885 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; PRIOR FILING DATE: 2004-04-23 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; NUMBER OF SEQ ID NOS: 33 ; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: Patentin version 3.3 ; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1 ; SEQ ID NO 40  
; LENGTH: 360 ; LENGTH: 544  
; TYPE: PRT ; TYPE: PRT  
; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens  
; US-11-112-304A-1 ; US-10-980-388-40

RESULT 22 ;  
US-10-980-388-40 ;  
; Sequence 40, Application US/10980388 ;  
; Publication No. US2005025490A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: Vogeli, Gabriel ;  
; APPLICANT: Parodi, Luis A. ;  
; APPLICANT: Hebsch, Ronald R. ;  
; APPLICANT: Lind, Peter ;  
; APPLICANT: Kovacs, Paul S. ;  
; APPLICANT: Ruff, Valerie ;  
; APPLICANT: Wood, Linda S. ;  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl ;  
; CURRENT FILING NUMBER: US/10/980, 388 ;  
; CURRENT FILING DATE: 2004-11-02 ;  
; PRIOR APPLICATION NUMBER: US/09/791, 932 ;  
; PRIOR FILING DATE: 2001-02-23 ;  
; PRIOR APPLICATION NUMBER: 60/184, 305 ;  
; PRIOR FILING DATE: 2000-02-23 ;  
; PRIOR APPLICATION NUMBER: 60/184, 304 ;  
; PRIOR FILING DATE: 2000-02-23 ;  
; PRIOR APPLICATION NUMBER: 60/184, 303 ;  
; PRIOR FILING DATE: 2000-02-23 ;  
; PRIOR APPLICATION NUMBER: 60/184, 397 ;  
; PRIOR FILING DATE: 2000-02-23 ;  
; PRIOR APPLICATION NUMBER: 60/184, 247 ;  
; PRIOR APPLICATION NUMBER: 60/184, 247 ;

QY 4 GLCTCQIKTGPAC 16 ;  
Db 56 GACTCCCTGTGC 68 ; PRIOR FILING DATE: 2000-02-23  
; Sequence 7, Application US/11096568A ; PRIOR APPLICATION NUMBER: 60/188, 880  
; Publication No. US2006004240A1 ; PRIOR FILING DATE: 2000-03-13  
; GENERAL INFORMATION: ; PRIOR APPLICATION NUMBER: 60/217, 369  
; APPLICANT: Alexandrov, Nickolai et al. ; PRIOR FILING DATE: 2000-07-11  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides ; PRIOR APPLICATION NUMBER: 60/217, 370  
; FILE REFERENCE: 2750-159RPS2 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; CURRENT APPLICATION NUMBER: US/11/096, 568A ; PRIOR APPLICATION NUMBER: 60/217, 370  
; CURRENT FILING DATE: 2005-04-01 ; PRIOR APPLICATION NUMBER: 60/217, 370  
; NUMBER OF SEQ ID NOS: 3447 ; NUMBER OF SEQ ID NOS: 3447  
; SEQ ID NO 24462 ; SEQ ID NO 24462  
; LENGTH: 839 ; LENGTH: 839  
; TYPE: PRT ; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays ; ORGANISM: Zea mays subsp. mays  
; FEATURE: ; FEATURE:  
; NAME/KEY: misc\_feature ; NAME/KEY: misc\_feature  
; LOCATION: (1)..(839) ; LOCATION: (1)..(839)  
; OTHER INFORMATION: Ceres Seq. ID no. 12435290 ; OTHER INFORMATION: Ceres Seq. ID no. 12435290  
; FEATURE: ; FEATURE:  
; NAME/KEY: misc\_feature ; NAME/KEY: misc\_feature  
; LOCATION: (325)..(325) ; LOCATION: (325)..(325)  
; OTHER INFORMATION: xaa is any aa, unknown or other ; OTHER INFORMATION: xaa is any aa, unknown or other  
; US-11-096-568A-24462 ; US-11-096-568A-24462

QY 1 LVGGTCAKRT 12 ;  
Db 437 LIGAGLICCAVRT 448 ;  
; Sequence 1, Application US/11096568A ;  
; Publication No. US2006004240A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: Alexandrov, Nickolai et al. ;  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides ;  
; TITLE OF INVENTION: Theby ;  
; FILE REFERENCE: 2750-159RPS2 ;  
; CURRENT APPLICATION NUMBER: US/11/096, 568A ;  
; CURRENT FILING DATE: 2005-04-01 ;  
; CURRENT FILING DATE: 2005-04-01

RESULT 24 ;  
US-11-096-568A-24461 ;  
; Sequence 1, Application US/11096568A ;  
; Publication No. US2006004240A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: Theby ;  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides ;  
; TITLE OF INVENTION: Theby ;  
; FILE REFERENCE: 2750-159RPS2 ;  
; CURRENT APPLICATION NUMBER: US/11/096, 568A ;  
; CURRENT FILING DATE: 2005-04-01 ;  
; CURRENT FILING DATE: 2005-04-01

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; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24461
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Zea maya subsp. maya
; FEATURE: misc_feature
; LOCATION: (1)..(878)
; OTHER INFORMATION: Ceres Seq. ID no. 12435289
; NAME/KEY: misc_feature
; LOCATION: (364)..(364)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; US-11-096-568A-24461

Query Match 45.6%; Score 41; DB 7; Length 878;
Best Local Similarity 50.0%; Pred. No. 57; Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVGLCITCQQIKT 12
Db 476 LLAGLICCAVRT 487

RESULT 25
US-11-096-568A-24460
Sequence 24460 Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 24460
LENGTH: 909
TYPE: PRT
ORGANISM: Zea maya subsp. maya
FEATURE: misc_feature
LOCATION: (1)..(909)
OTHER INFORMATION: Ceres Seq. ID no. 12435288
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (395)..(395)
OTHER INFORMATION: Xaa is any aa, unknown or other
; US-11-096-568A-24460

Query Match 45.6%; Score 41; DB 7; Length 909;
Best Local Similarity 50.0%; Pred. No. 59; Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVGLCITCQQIKT 12
Db 507 LLAGLICCAVRT 518

RESULT 26
US-11-114-962-1
Sequence 1 Application US/11114962
Publication No. US20060030694A1
GENERAL INFORMATION:
APPLICANT: Kitajewski, Jan
APPLICANT: Shawer, Carrie
APPLICANT: Funahashi, Yasuhiro
TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof
FILE REFERENCE: 0575//1308-A
CURRENT APPLICATION NUMBER: US/11/114,962
CURRENT FILING DATE: 2005-04-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.3

RESULT 27
US-11-050-346-67
Sequence 67 Application US/11050346
Publication No. US20060002924A1
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark William
APPLICANT: Champion, Brian Robert
APPLICANT: Lennard, Andrew Christopher
APPLICANT: McKenzie, Graham James
APPLICANT: Tugal, Tamara
APPLICANT: Ward, George Albert
TITLE OF INVENTION: CONTOURINE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
FILE REFERENCE: 674525-2016
CURRENT APPLICATION NUMBER: US/11/050,346
CURRENT FILING DATE: 2005-02-03
PRIOR APPLICATION NUMBER: GB 0312062-3
PRIOR FILING DATE: 2003-05-24
PRIOR APPLICATION NUMBER: PCT/GB03/01525
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: GB 0300234-2
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: GB 0218068-5
PRIOR FILING DATE: 2003-08-03
PRIOR APPLICATION NUMBER: PCT/GB03/01525
PRIOR FILING DATE: 2003-09-07
PRIOR APPLICATION NUMBER: GB 0220912-0
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: GB 0220913-8
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: PCT/GB02/05137
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/GB02/05133
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 67
LENGTH: 2556
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: mod_rss
LOCATION: (891)
OTHER INFORMATION: Variable amino acid
; US-11-050-346-67

Query Match 45.0%; Score 40.5%; DB 7; Length 2556;
Best Local Similarity 61.5%; Pred. No. 1. 8e+02; Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
Qy 5 ICLTCQI-KTGAC 16
Db 397 ICTCPGTYGPAC 409

RESULT 28
US-10-793-626-2510
Sequence 2510 Application US/10793626

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Publication No. US20050255478A1 ; CURRENT APPLICATION NUMBER: US/11/096, 051  
; GENERAL INFORMATION: ; CURRENT FILING DATE: 2005-03-30  
; APPLICANT: KIMMERLY, WILLIAM JOHN ; PRIOR APPLICATION NUMBER: 10/038, 854  
; TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEAR ACIDS AND PROTEINS ; PRIOR FILING DATE: 2001-12-31  
; FILE REFERENCE: PUS480US ; PRIOR APPLICATION NUMBER: 10/455, 772  
; CURRENT FILING DATE: 2004-03-04 ; PRIOR FILING DATE: 2003-06-04  
; PRIORITY APPLICATION NUMBER: 60/164, 258 ; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 38 ; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin Ver. 2.1 ; SOFTWARE: Curaseqlist version 0.1  
; SEQ ID NO: 2510 ; SEQ ID NO: 12  
; LENGTH: 205 ; LENGTH: 257  
; TYPE: PRT ; TYPE: PRT  
; ORGANISM: Artificial Sequence ; ORGANISM: Homo sapiens  
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic ; US-11-096-051-12  
; FEATURE: OTHER INFORMATION: amino acid sequence ;  
; NAME/KEY: MOD RES ;  
; LOCATION: (205) ;  
; OTHER INFORMATION: variable amino acid ;  
; US-10-793-626-2510 ;  
Query Match 44.4%; Score 40; DB 6; Length 205;  
Best Local Similarity 60.0%; Pred. No. 22; Mismatches 1; Indels 3; Gaps 0;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 4 GLCTCQIKNG 13  
Db 141 GLCYCDVSTG 150  
RESULT 29 ;  
US-10-894-592-3 ;  
; Sequence 3, Application US/10894592  
; Publication No. US20060019335A1  
; GENERAL INFORMATION:  
; APPLICANT: Du, Chunying  
; APPLICANT: Yang, Qi-Heng  
; TITLE OF INVENTION: Compositions and Methods to Promote c-IAP Autodegradation  
; FILE REFERENCE: 68175  
; CURRENT APPLICATION NUMBER: US/10/894,592  
; CURRENT FILING DATE: 2004-07-20  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO: 3  
; LENGTH: 1356  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-894-592-3  
Query Match 44.4%; Score 40; DB 6; Length 1356;  
Best Local Similarity 53.8%; Pred. No. 1.2e+02; Mismatches 6; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 4 GLCTCQIKNGPAC 16  
Db 893 GCCCTCTGGTC 905  
RESULT 30 ;  
US-11-096-051-12 ;  
; Sequence 12, Application US/11096051  
; Publication No. US20050244868A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: MacLachlan, Timothy K  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Varnet, Corine  
; APPLICANT: Ettenberg, Seth  
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use  
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